Title: Perfect score: Sequence:

Run on:

Scoring table:

Searched:

Database :

Sequence 1 sequence 1 sequence 1 sequence 1 sequence 1 sequence 1 sequence 2 sequence 2

Sequence 121, 1 Sequence 121, 1 Sequence 121, 1 Sequence 189, 1

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Sequence 20, Application US/0989046
| Bedication No. US20030008274A1 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: |
| TITLE OF INVENTION: | Genotypes for diagnosis, prophylaxis and therapy. |
| TITLE OF INVENTION: | Genotypes for diagnosis, prophylaxis and therapy. |
| TITLE OF INVENTION: | Genotypes for diagnosis, prophylaxis and therapy. |
| TITLE OF INVENTION: | Genotypes for diagnosis, prophylaxis and therapy. |
| TITLE OF INVENTION: | Genotypes for diagnosis, prophylaxis and therapy. |
| COMPUTER READABLE FORM: | Genotypes for diagnosis, prophylaxis and therapy. |
| COMPUTER: IBM PC compatible |
| FILING DATE: |
| PRIOR APPLICATION DATA: |
| FILING DATE: |
| PRIOR APPLICATION NUMBER: 08/362,455 |
| FILING DATE: |
| FILING DATE: |
| TYPE: amino acide |
| TOPOLOGY: |
| US-09-899-046-20
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US-10-128-587A-91

US-10-651-165-210

US-09-899-046-24

US-09-899-046-28

US-09-899-046-28

US-09-878-281-24

US-09-877-224-24

US-09-877-224-24

US-09-877-224-24

US-09-877-224-24

US-09-877-224-24

US-09-877-224-24

US-09-877-224-14

US-09-899-046-11

US-09-873-224-14

US-09-873-224-14

US-09-873-224-14

US-09-873-224-14

US-09-873-224-16

US-09-873-224-176

US-09-873-224-176

US-09-873-224-121
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Best Local Similarity 100.
Matches 180; Conservative
   US-09-899-046-20
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Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 30, Appl
                                                                                                                        December 1, 2004, 23:38:24; Search time 143 Seconds (without alignments) 448.896 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                              US-09-899-046A-20
964
1 VGAPVGGVARALAHGVRALE......TVQTCNCSLYPGHLSGHRMA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

| cgn2 6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/PCT_NEW_PUB_Pep:*
| cgn2 6/ptodata/2/pubpaa/PCT_NEW_PUB_Pep:*
| cgn2 6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US07_NEW_PUB_Pep:*
| cgn2 6/ptodata/2/pubpaa/US08_NEW_PUB_Pep:*
| cgn2 6/ptodata/2/pubpaa/US08_NEW_PUB_Pep:*
| cgn2 6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US10F_PUBCOMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-899-046-20
US-09-899-046-22
US-09-878-281-22
US-09-873-224-20
US-09-973-022-30
US-09-973-022-30
US-09-995-303-30
US-09-995-860-30
US-09-995-860-30
US-09-995-91
                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             1582122 seqs, 356623098 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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Gaps

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Result

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/878,281
FILING DATE:
PRIOR PAPEL STATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
      FILING DATE:
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
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amino acid
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Best Local Similarity 100.
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-878-281-20
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US-09-873-224-20
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| Publication No. US20030032005A1 |
| GENERAL INFORMATION: |
| APPLICANT: |
| TITLE OF INVENTION: |
| TITLE OF INVENTION: |
| GENERAL INFORMATION: |
| TITLE OF INVENTION: |
| GENOLOGIES |
| TITLE OF INVENTION: |
| TITLE OF INVENTION: |
| TITLE OF INVENTION: |
| GENOLOGIES |
| TITLE OF INVENTION: |
| TITL
                                61 LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
                                                                                                                         SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180
                                                                                                                                                             LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
GENOLOGYES:
270
COMPUTER READABLE FORM:
MEDIUM TYPE:
FLOPPY disk
COMPUTER:
DE-POSSYMEN:
OFFRATION SYSTEM:
OFFRATION SYSTEM:
APPLICATION DATA:
APPLICATION NUMBER:
US/09/899,046
FILING DATE:
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Best Local Similarity 100.0%; Pred. No. 1.7e-96;
Matches 180; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/09899046 Publication No. US20030008274A1 GENERAL INFORMATION:
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APPLICATION NUMBER: 08/362,455
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APPLICATION NUMBER: 08/362,455
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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US-09-899-046-22
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US-09-878-281-20
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                                                                                                                                                                                                                                                                                                                                       1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG 60
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Sequence 22, Application US/08878281

Fublication No. US20030032005A1

GENERAL INFORMATION:

APPLICANT:
APPLICANT:
TITLE OF INVENTION:

NUMBER OF SEQUENCES: 270

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PROPAMS:

COMPUTER: OF NOWENTER: POCOMPATIBLE

COMPATIBLE

COMPUTER: OF NOWENTER: POCOMPATIBLE

COMPATIBLE

COMPATI
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             Length 180;
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100.0%; Score 964; DB 10;
100.0%; Pred. No. 1.7e-96;
ive 0; Mismatches 0;
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61 LYVLINDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
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TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
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Best Local Similarity 100.0%; Pred. No. 1.7e-96;
Matches 180; Conservative 0; Mismatches 0; Indels 0.
SOFTWARE: PatentIn Release #1.0, Version #1.25
                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/873,224
FILING DATE: 05-Jun-2001
CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
FILING DATE: «Unknown»
ATTORNEY/AGENT INPORMATION:
NAME: Innogenetics sa.
TELECOMMUNICATION: NEPORMATION:
TELEPHONE: 00 32 9 241 07 11
TELEPHONE: 00 32 9 241 07 11
TELEPHONE: 00 32 9 241 07 99
INPORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-873-224-22
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APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
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APPLICATION NUMBER: US/09/973,025
FILING DATE: 10-00t-2001
CLASSIFICATION: <Unknown>
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Publication No. US20020182706A1
GENEAL INFORMATION:
APPLICANT: MAERTENS, GEERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 111
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DE MARTYNOFF,
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Sequence 22, Application No. US20030064360A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: <Unknown>
ITILE OF INVENTION: New sequences of hepatitis C virus
genotypes for diagnosis, prophylaxis and therapy.
NUMBER OF SEQUENCES: 270
                                                  GENERAL INFORMATION:

APPLICANT: <Unknown>
TITLE OF INVENTION: New sequences of hepatitis C virus
genotypes for diagnosis, prophylaxis and therapy.
NUMBER OF SEQUENCES: 270
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                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

ZIP: B-9052

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/873,224

FILING DATE: 05-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION NUMBER: 08/562,455

FILING DATE: UDKNOWN>

APPLICATION NUMBER: 08/562,455

FILING DATE: ADMINOWN>

ATTORNEY/AGENT INFORMATION:
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STREET: Industriepark Zwijnaarde 7, box 4
CITY: Ghent
COUNTY: Belgium
ZIP: B-9052
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
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100.0%; Pred. No. 1.7e-96;
tive 0; Mismatches 0;
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STREET: Industriepark Zwijnaarde 7, box
CITY: Ghent
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TELEPHONE: 00 32 9 241 07 11
TELEFAX: 00 32 9 241 07 99
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
TENGTH: 180 amino acids
TYPE: amino acids
     Application US/09873224
No. US20030064360A1
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Best Local Similarity
          Sequence 20, App. Publication No.
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US-09-873-224-22
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us-09-899-046a-20.rapb

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RESULT 9
US-09-995-808-30
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LENGTH: 208
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BOSMAN, FONS

DE MARTYNOFF, GUY

BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE

PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTRY: VIEGUIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FO Compatible
COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 964; DB 9; Length 208; 100.0%; Pred. No. 2.1e-96; tive 0; Mismatches 0; Indels
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ADDRESSER: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
REFERENCE/DOCKET NUMBER: 1487-10
                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
CLENGTH: 208 amino acids
TYPE: amino acid
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Publication No. US20030036110A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 180; Conservative
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US-09-899-303-30
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Sequence 30, Application US/09998808
Publication No. US20300959804
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
TITLE OF INVENTION: therapeutic use.
FILE REFERENCE: 2551-70
CURRENT APPLICATION NUMBER: US/09/995,808
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PATENTIA 3.1
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US-09-995-860-30
US-09-995-860-30
US-09-995-860-30
Sequence 30, Application US/0995860
Sequence 30, Application No. US2030118603A1
SEQUENCE INFORMATION:
TITLE OF INVENTION: Durified hepatitis C virus envelope proteins for diagnostic and TITLE OF INVENTION: therapeutic use.
TITLE REPERRNCE: 2551-69
CURRENT APPLICATION NUMBER: US/09/995,860
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 122
SOCTHARB: Patentin 3.1
SEQ ID NO 30
LENGTH: 208
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                                                                                                                                             Length 208;
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                                                                                                                                             100.0%; Score 964; DB 10;
100.0%; Pred. No. 2.1e-96;
tive 0; Mismatches 0;
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) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-899-303-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Hepatitis C virus US-09-995-808-30
                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 180; Conservative
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Sequence 9.7 Application US/10128587A
Publication No. US20030152940A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelope
TITLE OF INVENTION: Droteins
TITLE OF INVENTION: Droteins
TITLE OF INVENTION: Droteins
TITLE OF INVENTION: Droteins
CURRENT APPLICATION NUMBER: US/10/128,587A
CURRENT FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin version 3.1
SEQ ID NO 91
LENGTH: 209
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                                                                                                                                                     Length 208;
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Publication No. US20030108561A1
GENERAL INFORMATION:
APPLICANT: Inmognetics N.V.
TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
FILE REFREENCE: 135 PCT
CURRENT APPLICATION WNOBER: US/10/128,590
CURRENT FILING DATE: 2002-07-22
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin version 3.1
SEQ ID NO 91
LENGTH: 209
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                                                                                                                                                  Query Match 100.0%; Score 964; DB 16; Best Local Similarity 100.0%; Pred. No. 2.1e-96; Matches 180; Conservative 0; Mismatches 0;
; SEQ ID NO 30
; LENGTH: 208
; TYPE: PT
; ORGANISM: Hepatitis C virus
US-10-321-798-30
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ORGANISM: hepatitis C virus

US-10-128-590-91
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Best Local Similarity
Matches 180; Conserv
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US-10-128-587A-91
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US-10-128-590-91
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Publication No. US20030147918A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and TITLE OF INVENTION: therapeutic use.

FILE REFERENCE: 2551-68

CURRENT APPLICATION NUMBER: US/09/995,791

CURRENT FILING DATE: 2001-11-29

SOFTWARE: PATENTIN 3.1

SEQ ID NO 30

LENGTH: 208
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Publication No. US20040126395A1
GENERAL INFORMATION:
FULL INFORMATION:
FILE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and TITLE OF INVENTION: therapeutic use.
FILE REPRESENCE: 2551-93
CURRENT FILIATIO NUMBER: US/10/321,798
CURRENT FILIATION NUMBER: 60/418,358
PRIOR APPLICATION NUMBER: 60/418,358
PRIOR APPLICATION NUMBER: 10/020,510
PRIOR PILING DATE: 2002-10-16
PRIOR PILING DATE: 2001-10-16
PRIOR PILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-10-18
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin 3.1
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                                                                            100.0%; Score 964; DB 10; Length 208; 100.0%; Pred. No. 2.1e-96; ive 0; Mismatches 0; Indels 0;
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100.0%; Score 964; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.1e-96;
Matches 180; Conservative 0; Mismatches 0;
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US-09-995-791-30
  ; ORGANISM: Hepatitis C virus US-09-995-860-30
                                                                         Query Match
Best Local Similarity 100.
Matches 180; Conservative
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US-09-995-791-30
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us-09-899-046a-20.rapb

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APPLICANT: LEROUX-ROBLS, Robert
APPLICANT: DELEXS, Robert
TYLLE OF INVENTION: LEADUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: URBER: US/10/651,165
FILES REFERENCE: 2521.94
CURRENT APPLICATION NUMBER: US/08/974,690C
PRIOR APPLICATION NUMBER: US/08/974,690C
PRIOR PILING DATE: 1997-11-19
PRIOR PILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
PRIOR PILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR PILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
SEQ ID NO 210
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; -FBATUME:
; OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus
US-10-128-587A-91
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100.0%; Score 964; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.1e-96;
Matches 180; Conservative 0; Mismatches 0;
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Sequence 210, Application US/10651165
Publication No. US20040047877A1
; CENERAL INFORMATION:
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; ORGANISM: hepatitis C virus
US-10-651-165-210
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Sequence 20, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 210, Appl
Sequence 200, Appl
Sequence 20, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 28, Appl
Sequence 208, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 207, Appl
Sequence 207, Appl
Sequence 21, Appl
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1 VGAPVGGVARALAHGVRALE.....TVQTCNCSLYPGHLSGHRMA 180
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6: /ognlo.6/ptodata1/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-878-281A-22
US-08-635-886C-210
US-08-635-886C-210
US-08-927-597-30
US-08-635-886C-210
US-08-974-690C-209
US-08-978-281A-24
US-09-878-281A-26
US-09-878-281A-28
US-09-878-281A-28
US-09-878-281A-14
US-09-878-281A-18
US-09-878-281A-18
US-08-974-690C-209
US-08-974-690C-207
US-08-974-690C-207
US-08-974-690C-207
US-08-974-690C-211
US-08-974-690C-2211
US-08-974-878-281A-175
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                                                                                                                                                                                                                                                                                            478139 segs, 66318000 residues
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                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 protein search, using sw model
                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                      US-09-899-046A-20
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                Copyright
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Match
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                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                            Searched:
                                                                                                  Run on:
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1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	450 4 US-08-974-690C-189 Sequence 189, App 450 4 US-08-635-886C-188 Sequence 188, App 5.0 450 4 US-08-635-886C-188 Sequence 188, App 5.1 450 4 US-08-974-690C-188 Sequence 188, App 5.1 3 US-08-878-281A-182 Sequence 182, App 5.1 3 US-08-034-756-20 Sequence 20, Appl 5.1 3 US-08-188-281B-13 Sequence 20, Appl 6.2 57 1 US-08-188-281B-13 Sequence 13, Appl 6.2 57 5 PCT-US95-01087-13 Sequence 13, Appl 6.4 5 PCT-US95-01087-13 Sequence 12, Appl 6.4 5 PCT-US95-01087-12 Sequence 1, Appl 6.4 5	ALIGNMENTS	ication US/09878281A ON:	100.0%; Score 964; DB 4; Length 180; rity 100.0%; Pred. No. 8e-104; nservative 0; Mismatches 0; Indels 0; Gaps 0;	VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG 60 	LYVLTNDGSNSSIVYEADDVILHTPGCIPCVQDGNTSTGWTPVTFTVAVKXVGATTASIR 120 	SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHOTVQTCNCSLYPGHLSGHRMA 180 	SULT 2 -09-878-281A-22 Sequence 22, Application US/09878281A Sequence 22, Application US/09878281A Sequence 22, Application US/09878281A SEMENAL INFORMATION: APPLICANT: Innogenetics N.V. APPLICANT: Innogenetics N.V. TITLE OF INVENTION: and therapy FILE REFERENCE: 35 CURRENT APPLICANTION NUMBER: US/09/878,281A CURRENT APPLICANTION NUMBER: US/09/878,281A NUMBER OF SEQ ID NOS: 284 SEQ ID NOS: 284 SEQ ID NO 22
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	77777777777777777777777777777777777777		-20 Applicatic 7-5024 7-5024 7-5024 7-5024 Tinnogenetic 7-30710N: Ne 7-30710N: Ne 7	lmilarity ; Conservat	/GAPVGGVARA /GAPVGGVARA	CYVLTNDCSNS	SHVDLLVGAAT SHVDLLVGAAT	22 Applicatio 662024 MATION: Innogenetic ENTION: Ne TENTION: Ne TCE: 35 TCE: 35 TO NO NO TO NO NO TO N
			S-09-878-281A- S-09-878-281A- Sequence 20 Patent No. 67 GENERAL INFORM TITLE OF INV TITLE OF INV TITLE OF INV CURRENT FILL CURRENT FILL NUMBER OF SE SCOTWARE: P SCOTTWARE: P SCOTTWARE: P CURRENT FILL NUMBER OF SE SCOTTWARE: P	Query Match Best Local Si Matches 180;				ULT 2 09-878-281A- equence 22, atent No. 67 atent No. 67 APPLICANT: I TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE REFEREN CURRENT APPL CURRENT FILL NUMBER OF SE SOFFWARE: PA

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61 LYVLTNDCSNSSIVYEADDVILHTFGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 208 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-927-597-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                            121 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA
                                                                                                                                                               Gaps
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                                                                                                                    Length 180;
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CITY: ARLINGTON
STATE: VIRGINIA
COUNTER: VIRGINIA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLAD PRO COMPATIBLE
COMPUTER: BLAD PRO COMPATIBLE
COMPUTER: BLAD PRO COMPATIBLE
SOFTWARE: PALENTIN RELEASE #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATE:
FLING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNIY/AGENT INFORMATION:
NAME: BYENE, THOMAS E: 1487-10
TELECOPHOLICATION INFORMATION:
TELECOPHOLICATION INFORMATION:
TELECOPHOLICATION INFORMATION:
TELECOPHORE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 minno acids
                                                                                                                                                             Indels
                                                                                                                 Query Match
100.0%; Score 964; DB 4;
Best Local Similarity 100.0%; Pred. No. 8e-104;
Matches 180; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/08612973;
Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: BOSMAN, FONS
APPLICANT: BD MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
ITTLE OF INVENTION: PURIFIED HEPATITIE
ITTLE OF INVENTION: PROTEINS FOR DIAGN
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERIYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: 208 amino acids amino acid
         ; LENGTH: 180
; TYBE: PRT
; -ORGANISM: hepatitis C virus
US-09-878-281A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 180; Conserv
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                                                                                                      1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
82 LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MAERTENSF, GUY
APPLICANT: DE WARSTWOFF, GUY
APPLICANT: DE WARSTWOFF, GUY
APPLICANT: DE WARSTWOFF, GUY
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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Best Local Similarity 100.0%; Pred. No. 9.9e-104;
Matches 180; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOWAS E.
REGISTRATION NUMBER: 32,205
REFENDE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                               RESULT 4
US-08-927-597-30
; Sequence 30, Application US/08927597
; Patent No. 6245503
; GENERAL INFORMATION:
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  Sequence 210, Application US/08635886C

| Ratent No. 6555114
| GENERAL INFORMATION:
| APPLICANT: LEROUX-ROELS, Geert
| APPLICANT: DELEYS, Robert
| TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
| TITLE OF INVENTION: MADER: US/08/635,886C
| TITLE OF INVENTION: MADER: US/08/635,886C
| CURRENT APPLICATION NUMBER: PCT/EP94/03555
| PRIOR APPLICATION NUMBER: PCT/EP94/03555
| PRIOR APPLICATION NUMBER: EP 93402718.6
| WINDER OF SEQ ID NOS: 286
| NUMBER OF SEQ ID NOS: 286
| SOFTWARE: Patentin version 3.1
| LENGTH: 193
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US-08-974-690C-210
US-08-974-690C-210
Sequence 210, Application US/08974690C
Fatent No. 661333
GENERAL INFORMATION:
APPLICANT: LERENUX-NELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: MAERIENS, Geert
TITLE OF INVENTION: URUS
FILE REFERENCE: 2551-94
FILE REFERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/08/974,690C
CURRENT FILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-0-28
PRIOR PLILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1994-10-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 960; DB 4; I
Pred. No. 2.6e-103;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.9%;
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: hepatitis C virus
US-08-635-886C-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-974-690C-210
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LENGTH: 193
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Sequence 209, Application US/08974690C

Sequence 209, Application US/08974690C

Patent No. 6613333

GENERAL INFORMATION:
APPLICANT: LEROWA-RELS, Geart
APPLICANT: DELEYS, Robert

APPLICANT: DELEYS, Robert

APPLICANT: MAERIENS, Geart

APPLICANT: WARNION: UNMODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNMODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNMOBER: US/08/974,690C

CURRENT FILING DATE: 1994-11-19

PRIOR APPLICATION NUMBER: PCT/EP94/03555

PRIOR APPLICATION NUMBER: EP 93402718,6

PRIOR APPLICATION NUMBER: 1993-11-04

NUMBER: OF SEQUENCE: 286

NUMBER: OF SECUENCE: 286

NUMBER: OF
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                                             74 LYVLTNDCSNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTPVTPTVAVRYVGATTASIR 133
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US-08-615-886C-209
US-08-615-886C-209
Sequence 209, Application US/08635886C
Patent No. 6555114
GENERAL INFORMATION:
APPLICANT: LEBENG. Geert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VARUE
TITLE OF INVENTION: VARUE
FILE REFERENCE: 2752-18
CURRENT FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR PILING DATE: 1993-11.04
NUMBER OF SEQ ID NOS: 286
SEQ ID NO 209
LENGTH: 187
LENGTH: 187
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Pred. No. 1.6e-102;
1; Mismatches 1;
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SEQ ID NO 209
LENGTH: 187
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Best Local Similarity 98.9%;
Matches 178; Conservative
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; ORGANISM: hepatitis C virus
US-08-635-886C-209
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US-08-974-690C-209
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APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophy
TITLE OF INVENTION: and therapy
TITLE OF INVENTION: and therapy
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
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Squence 208, Application US/08635886C

CENERAL INFORMATION:
APPLICANT: LEROUX-ROBILS, Geert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: URUS
FILE REFERENCE: 272-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT APPLICATION NUMBER: US/08/635,886C
PRIOR APPLICATION NUMBER: US/08/635,886C

PRIOR APPLICATION NUMBER: 1996-04-25
PRIOR APPLICATION NUMBER: EP944/03555
PRIOR PELLING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
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                                                                 Length 180;
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                                                               98.7%; Score 951; DB 4; L
ilarity 97.8%; Pred. No. 2.6e-102;
Conservative 2; Mismatches 2;
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; ORGANISM: hepatitis C virus US-09-878-281A-26
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Matches 176, Conservative
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US-08-635-886C-208
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US-09-878-281A-28
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US-09-878-281A-28
                                                                                          Best Local Sim
Matches 176;
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Patent No. 6762024
GENERAL INFORMATION:
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph TITLE OF INVENTION: and therapy
FILE DE INVENTION and therapy
FILE REPERBNE: 35
CURRENT FILING DAFE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 180
TYPE: PRT
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TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
FILLE OF INVENTION: and therapy
FILLE REFERENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILLING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
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                                                                                            Length 187
                                                                                                                                      1; Indels
                                                                                          Score 953; DB 4; I
Pred. No. 1.6e-102;
1; Mismatches 1;
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                                                                                       98.9%;
milarity 98.9%;
Conservative 1
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, ORGANISM: hepatitis C virus
US-09-878-281A-24
  ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-C8-974-690C-209
                                                                                            Query Match
Best Local Similarity
Matches 178; Conserv
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US-09-878-281A-26
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Patent No. 6613333

GENERAL INFORMATION:

APPLICANT: LEROUX-ROELS, Gert

APPLICANT: DELEYS, Robert

APPLICANT: DELEYS, Robert

TITLE OF INVENTION: INMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: INMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: INMUNDER: US/08/974,690C

URRENT APPLICATION NUMBER: US/08/974,690C

CURRENT APPLICATION NUMBER: US/08/9741696

PRIOR APPLICATION NUMBER: P93402718.6

PRIOR PILING DATE: 1993-11-04

NUMBER OF SEQ ID NOS: 286

SOFTWARE: PARENTIN VERSION 3.1

SEQ ID NO 2 BEENTIN VERSION 3.1
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                                                                                                                                                                            Length 187;
                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                         Score 951; DB 4; I
Pred. No. 2.7e-102;
2; Mismatches 2;
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US-09-878-281A-14
Sequence 14, Application US/09878281A
Patent No. 6762024
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
SEQ ID NO 208
                                                                                                                                                                         Query Match
Best Local Similarity 97.8%;
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: hepatitis C virus US-08-974-690C-208
                                                                                  ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-208
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US-08-974-690C-208
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Patent No. 6762024
GENERAL INFORMATION:
Patent No. 6762024
GENERAL INFORMATION:
TITLE OF INVENTION: New Sequences of hepatitis C virus genotypes for diagnosis, proph;
TITLE OF INVENTION: and therapy
FILE REPEBENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT PILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOUTHARE: Patentin version 3.1
sequences of hepatitis C virus genotypes for diagnosis, prophy
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Pred. No. 5.8e-102;
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Pred. No. 5.8e-102;
3; Mismatches 2;
TITLE OF INVENTION: New sequences of hepatiti;
TITLE OF INVENTION: and therapy
FILE REPERENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH: 180
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ilarity 97.2%;
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; ORGANISM: hepatitis C virus
US-09-878-281A-14
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

protein search, using sw model 1 OM protein December 1, 2004, 23:26:38; Search time 152 Seconds (without alignments) 424.811 Million cell updates/sec Run on:

US-09-899-046A-20 964 1 VGAPVGGVARALAHGVRALE......TVQTCNCSLYPGHLSGHRMA 180 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

2002273 seqs, 358729299 residues Searched:

2002273

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	0 Polypept:	Н	18670	Add55538 Hepatitis	20	561 Hepatit	374	82	4	283	279	277	Aar63278 Polypepti	62	65 Hepatit	32	00	22 Infectio	170 Amino a	27 Hepatit	9401	3021	4067 N	Aar98362 5'UTR/COR	Aaw68461 Protein e
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AAW68465 AAR24087 AAM47264	AAR38279 AAW68466 AAB59174	AAR63368 AAR20723 AAR20720	AAR34478 AAR34477	AAR34476 AAE00449	AAW77398 AAU99290	AAO26784 ABU61849	AAR25115 AAR79222	AAW12715
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ALIGNMENTS

Polypeptide encoded by hepatitis C virus Core/El sequence. AAR63280 standard; protein; 180 AA. (revised)
(first entry) 25-MAR-2003 01-AUG-1995 AAR63280; RESULT 1 AAR63280

Hepatitis C virus; HCV; primer; probe; detection; diagnosis; classification; immunisation; prophylaxis; serotyping.

Hepatitis C virus type 3a.

WO9425601-A2

10-NOV-1994.

94WO-EP001323 27-APR-1994;

93EP-00401099. 93EP-00402019. 27-APR-1993; 05-AUG-1993;

(INNO-) INNOGENETICS NV SA.

ï Maertens G, Stuyver

WPI; 1994-358277/44. N-PSDB; AAQ78032.

New polynucleotide sequences from hepatitis C virus - and related vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates.

Claim 11; Page 110-111; 404pp; English.

Compositions comprising at least 5, and pref. 8 or more contiguous nuclectides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the Core/El region of HCV subtype 33; (1i) the region spanning positions 4664-4730 of the NS3 region of HCV type 3; (1ii) the region spanning positions 4692-5292 of the NS3/4 region of HCV type 3; (iv) the region spanning positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype 3; or (v) an HCV subtype 3 cy genomic sequence, may be used as primers to amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid.

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Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Core/El region of HCV subtype 3a and is taken from a clone designated BR36-9-13. (Updated on 25-MAR-2003 to correct PN field.)
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100.0%; Pred. No. 4.7e-95;
tive 0; Mismatches 0; Indels (
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classification; immunisation; prophylaxis; serotyping.
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93EP-00402019.
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(first entry)
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                                                                                                                                                                      Similarity
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                                                                                                                Sequence 180 AA;
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05-AUG-1993;
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01-AUG-1995
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Matches 180;
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                                                                                                                                                                                                                                                                                 LYVLINDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
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Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Core/El region of HCV subtype 3a and is taken from a clone designated BR36-9-20. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                            Length 180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 183; 243pp; English.
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30-AUG-2001; 2001US-0315768P.
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                                                                                                                                                       Local Similarity
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                                                                                                          Sequence 180 AA;
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ö LYVLTNDCSNSSIVYBADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180 81 treatment of patients suffering from HCV infection. The present sequence is a protein described in the exemplification of the invention The invention comprises an Hepatitis C virus (HCV) vaccine for reducing liver disease. The vaccine of the invention comprises an HCV El or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present amino acid sequence represents an HCV El/E2 protein. Hepatitis C virus; HCV; vaccine; liver disease; El protein; E2 protein; liver fibrosis. 1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG New hepatitis C virus (HCV) vaccine composition, useful for reducing liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal ö Length 208; Score 964; DB 5; Length 2 Pred. No. 5.7e-95; Mismatches 0; Indels 100.0%; Score 964; DB 7; 1larity 100.0%; Pred. No. 5.7e-95; Conservative 0; Mismatches 0; Disclosure, SEQ ID NO 30, 271pp; English. Hepatitis C virus E1/E2 protein #5. ADD55538 standard; protein; 208 AA. Bosman F; 0; 100.0%; 2001US-00020510. 2002US-0418358P. 18-DEC-2002; 2002WO-EP014480 180; Conservative (INNO-) INNOGENETICS NV Depla E, WPI; 2003-541632/51. N-PSDB; ADD55537. Similarity Hepatitis C virus. Sequence 208 AA; AA; WO2003051912-A2. 18-DEC-2001; 16-OCT-2002; Sequence 208 15-JAN-2004 Maertens G, 26-JUN-2003 22 61 82 121 ADD55538; Query Match Best Local Matches RESULT 4 ADD55538 88333 g g ò ठे ò

18-DEC-2001; 2001US-0453708P. 16-OCT-2002; 2002US-0418358P. 18-DEC-2002; 2002US-00321798

(MAER/) MAERTENS G. (DEPL/) DEPLA E. (BOSM/) BOSMAN F.

121 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180

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ADP71120 standard; protein; 208

(first entry)

23-SEP-2004

ADP71120;

HCV El protein HCC162.

82 LYVLINDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR

LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR

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원 8 셤 Hepatitis C virus, HCV; El glycoprotein; El glycoprotein; HCV infection; liver disease; liver fibrosis; immunogen; serum alanine aminotransferase level; steatosis; anti-El immunoreactivity; vaccine.

Hepatitis C virus; type 3a

US2004126395-A1.

01-JUL-2004

141

The invention relates to the use of a hepatitis C virus (HCV) vaccine composition for reducing liver disease (such as liver fibrosis or its progression), serum alanine aminotransferase (ALT) levels, steatosis, or anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal, or for treating a chronic HCV-infected mammal. The liver disease is reduced by at least 1-2 points according to the overall Ishak score in the HCV-infected mammal. Also included mammal. The liver disease is changes in liver disease in a chronic HCV-infected mammal, a therapeutic HCV vaccine composition (comprising at least one purified or a combination of at least 2 HCV single or specific oligomeric recombinant envelope protein selected from an El or E2 protein, a part of El and E2 protein, an El/E2 protein complex formed from purified HCV single or specific oligomeric recombinant El or E2 protein, a part of El and E2 composition (comprising at least one El or E2 peptide, and optionally, a pharmaceutical adjuvant), and composition (comprising a recombinant virus allowing expression of at least one HCV recombinant envelope protein (selected from an E1 protein and/or an E2 protein, and CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV caposition (comprising a recombinant virus allowing expression of at least one HCV recombinant envelope protein (comprising a recombinant virus allowing expression of at least one HCV recombinant envelope protein composition (comprising a recombinant virus allowing expression of the E1 and E2 proteins and, Use of hepatitis C virus (HCV) vaccine composition for reducing liver disease, serum alanine aminotransferase levels, steatosis, or anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal. Example 2; SEQ ID NO 30; 176pp; English. Ľ, Depla E, WPI; 2004-499089/47. N-PSDB; ADP71119. Maertens G,

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Gaps

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Indels

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Query Match Best Local Similarity Matches 180; Conserv

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Length 208;

9

1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG

the host cell is capable of expressing the protein cited above. (I) has heparctropic, virucide and antiinflammatory activities, and can be used in gene therapy and vaccines. The recombinant nucleic acid is useful for efficient expression of Hepartics C virus envelope proteins in eukaryotic cells, such as yeast cells. The HCV envelope proteins may be used as a nati-HCV antibodies, and/or genotyping of HCV, for prognosing or monitoring of HCV disease, or as a therapeutic agent. The method is used to producing HCV envelope protein or its part in a host cell. ABQ84197 to ABQ8423 and ABPS5528 to ABPS5568 represent sequences used in the exemplification of the present invention

9

Gaps

6

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100.0%; Score 964; DB 6; 100.0%; Pred. No. 5.7e-95; ive 0; Mismatches 0;

Query Match
Best Local Similarity 100.
Matches 180; Conservative

Sequence 209 AA;

Length 209; Indels 1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG

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optionally, a pharmaceutical adjuvant. The HCV vaccine composition is useful for reducing liver disease (such as liver fibrosis or its progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in the liver in a chronic HCV-infected mammal, or for treating a chronic HCV-infected mammal, or for treating a chronic HCV in in vitro monitoring HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is an HCV E1 protein (or fragment).
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antiinflammatory; gene therapy; vaccine.
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Pred. No. 5.7e-95;
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Best Local Similarity 100.0%;

Matches 180; Conservative 0
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17-JUL-2001; 2001US-0305604P.
                                                                                                Van Broekhoven A,
                                                                                         (INNO-) INNOGENETICS NV
                                                                                                        WPI; 2003-093095/08.
                                                Hepatitis C virus
                                                       WO200285932-A2.
                                                               31-OCT-2002
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61 LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120 142 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 202 23 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG 82 LYVLTNDCSNSSIVYBADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR Hepatitis C virus, HCV, envelope protein, virucide, immunostimulant, immune response, T-cell, therapy, infection, pharmaceutical, vaccine Samson I; Suckow M, ŭ Sablon Z Deschamps G, AAE32874 standard; protein; 209 24-APR-2002; 2002WO-BE000064. 24-APR-2001; 2001EP-00870088. 17-JUL-2001; 2001US-0305604P. Hepatitis C virus protein #9. (INNO-) INNOGENETICS NV Bosman A, WPI; 2003-103409/09. Hepatitis C virus. WO200286101-A2. 24-MAR-2003 Ö 31-OCT-2002 Depla E, | Verheyden (83 121 AAE32874; 143 RESULT 7 AAE32874 g 셤 $\dot{\circ}$ 8

The invention relates to Hepatitis C virus (HCV) envelope protein with N-glycosylation site(s). The HCV envelope protein, or the pharmaceutical composition comprising the envelope protein, is useful as a medicament or a vaccine, particularly for inducing a HCV-specific immune response. Claim 10; Page 343-344; 355pp; English.

The present invention describes a recombinant nucleic acid (I) comprising a nucleotide sequence encoding a protein having an avian lysozyme leader peptide, or its functional equivalent, joined to a Hepatitis C virus (HCV) envelope protein or its part. Also described: (I) a vector comprising the recombinant nucleic acid; (2) a host cell comprising the recombinant nucleic acid; (2) a method for producing HCV envelope protein or its part in a host cell, comprising transforming the host cell with the recombinant nucleic acid or where we have the vector, where

New Hepatitis C virus (HCV) envelope protein with N-glycosylation site(s), useful as a vaccine for inducing a HCV-specific immune response or HCV-specific antibodies, particularly for preventing or treating HCV infection.

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envelope proteins in eukaryotic cells, comprising a sequence encoding protein having an avian lysozyme leader peptide joined to the HCV

recombinant nucleic acids for

Claim 5; Page 310-311; 319pp; English.

envelope protein.

expressing Hepatitis C virus (HCV)

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inducing HCV-specific antibodies or inducing a T-cell function in a mammal. The protein is particularly useful for preventing, treating or diagnosing HCV infection. It is also useful for detecting the presence anti-HCV antibodies in a sample. The present sequence is Hepatitis C virus protein used in the invention
                                                                                                                                                 1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
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100.0%; Pred. No. 5.7e-95;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 180; Conservative
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N-PSDB; AAQ78034.
                                                                           Sequence 209 AA;
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01-AUG-1995
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Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV. for the detection of antibodies directed against HCV and for serctyping. This sequence corresponds to the Core/El region of HCV subtype 3a and is taken from a clone designated BR33-1-10. (Updated on 25-MAR-2003 to correct PN field.)
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Pred. No. 1.2e-93;
2; Mismatches 2;
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N-PSDB; AAQ78036.
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N-PSDB; AAQ78031.
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Best Local 2
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                                                                                                                                                                                            61 LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                           SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180
                                                                                                                                                                                                                                                              SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180
Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Core/E1 region of HCV subtype 3a and is taken from a clone designated BR33-1-20. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                             1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
                                                                                                                                                               VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAAGLEWRNTSG
                                                                                                                                                                                                          LYVLTNDCSNSSIVYEADDVILHAPGCVPCVQDGNTSTCWTPVTPTVAVRYVGATTASIR
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                                                                                                Length 180
                                                                                                                                                                                                                                                                                                                                                                                                             encoded by hepatitis C virus Core/El sequence.
                                                                                                                       2; Indels
                                                                                                Score 951; DB 2;
Pred. No. 1.2e-93;
                                                                                                                       2; Mismatches
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93EP-00402019.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus type 3a
                                                                                                          al Similarity 97.8
176; Conservative
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                                                                         Sequence 180 AA;
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05-AUG-1993;
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01-AUG-1995
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Best Local
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Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serctyping. This sequence corresponds to the Core/E1 region of HCV subtype 3a and is taken from a clone designated BR33-1-19. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LYVLTNDCSNSSIVYEADDVILHAPGCVPCVQDGNTSTCWTPVTPTVAVRYVGATTASIR
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                                                                                                                                                                                                                                                                            Length 180
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                                                                                                                                                                                                                                                                         Score 951; DB 2;
Pred. No. 1.2e-93;
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                                                                                                                                                                                                                                                                            98.7%;
97.8%;
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(first entry)
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Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (i) the region spanning positions 47-557 of the Core/E1 region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 4664-4730 of positions 8023-825 of the NS3/4 region of HCV type 3; (iv) the region spanning positions 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primars to amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid.
                                                                                                                                                                                                                                                                                                                              SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180
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                                                                                                                                                                                                                                                                 LYVLTNDCSNSSIVYBADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
                                                                                                                                                                                                                                                                                    61 LYVLINDCSNSSIVYEADDVILHTPGCVPCVQDGNTSACWTPVTPTVAVRYVGATTASIR 120
for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Care/El region of HCV subtype 3a and is taken from a clone designated HD10-2-21. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                         1 VGAPVGGVARALAHGVRALEDGINFATGNLFGCFSIFLLALFSCLIHPAASLEWRNTSG
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                                                                                                                                    Length 180;
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                                                                                                                     Score 948; DB 2; Length 10. Pred. No. 2.5e-93;
                                                                                                                                                                      3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR63277 standard; protein; 180 AA
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93EP-00402019
                                                                                                                                       98.3%;
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(first entry)
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                                                                                                                                                     Similarity
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                                                                                                          Sequence 180 AA;
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20-JUL-1995
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Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the Core/E1 region of HCV type 3; (ii) the region spanning positions 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 4692-5292 of the NS3/4 region of HCV type 3; (iv) the region spanning positions 9023-8235 of the NS5 region of the BR36 subgroup of HCV subtype 3; (v) an HCV subtype 3c genomic sequence, may be used as primers to amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid.
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Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for servicing. This sequence corresponds to the Core/El region of HCV subtype 3a and is taken from a clone designated HDI0-2-5. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                    Length 180;
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                                                                                                                                    Score 948; DB 2; Length 18
Pred. No. 2.5e-93;
3; Mismatches 2; Indels
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                                                                                                                                     98.3%;
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93EP-00402019.
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(first entry)
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                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                          Sequence 180 AA;
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21-JUL-1995
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                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                  121 RHVDILVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180
                                                                                                                                                                                                                                        LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for servyping. This sequence corresponds to the Core/31 region of HCV subtype 3a and is taken from a clone designated HDI0-2-14. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C virus genomic RNA, DNA and related proteins - useful for diagnosis and identification of hepatitis C virus sub-type.
                                                                                                                                                                               1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification.
2433. .2448
//note= "this part of the sequence is missing from the specification"
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/note= "this part of the sequence is missing from
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                                                                                                                     Length 180;
                                                                                                                                                 Indels
                                                                                                                     Score 941; DB 2; Le
Pred. No. 1.4e-92;
3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                      AAR94462 standard; protein; 3023 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus polypeptide
                                                                                                                      97.6%;
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                                                                                                                 Query Match
Best Local Similarity 96.7
Matches 174; Conservative
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N-PSDB; AAT13279.
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detection, diagnos
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                                                                                          Sequence 180 AA;
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                                                                                                                            199
                                                                                                                                                             119
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                                                                                                                                                                                                                                          260 RNHVNMLVAPPTLCSALYVEDAFGAVSLVGQAFTFRPRQHKTVQTCNCSIYPGHVSGHRM 319
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                                                                                          1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
                                                                                                                 61 LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQ-DGNTSTCWTPVTPTVAVKYVGATTASI
                                                                                                                                                                                                                            120 RSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide sequences from hepatitis C virus - and relate vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates.
                                                             ..
                           Length 3023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus, HCV, primer, probe, detection, diagnosis, classification, immunisation, prophylaxis, serotyping.
                                                             Indels
                             DB 2;
                                                                16;
                             81.4%; Score 784.5; DB 279.0%; Pred. No. 3.5e-74;
                                                           21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 225-226; 404pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              AAR63365 standard; protein; 193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus El polypeptide.
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93EP-00402019.
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(first entry)
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                                             Similarity
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Sequence 3023 AA;
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Best Local Simil
Matches 143; (
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05-AUG-1993;
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15-AUG-1995
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Search completed: December 1, 2004, 23:40:54 Job time : 155 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 1, 2004, 23:45:01; Search time 38 Seconds (without alignments) 455.764 Million cell updates/sec Run on:

US-09-899-046A-20 180 1 VGAPVGGVARALAHGVRALE......TVQTCNCSLYPGHLSGHRMA 180 OLIGO Gapop 60.0 , Gapext 60.0 Title: Perfect score: Scoring table: Sequence:

283416 seqs, 96216763 residues Searched:

0 Word size :

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

PIR_79;*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description								enoue	genome polyprotein	polyprotein - hepa	χç		genome polyprotein		genome polyprotein	structural protein	genome polyprotein		enone				ypothe	genome polyprotein			enone	enome polyprot	genome polyprotein
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GNWVC3 GNWVCH S40770	GNWVJ8 PC4407 JQ1925	JQ1926 S32749 PN0011	PC2219 S32745 S32743	PS0164 S32746	S32741 S25123
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ALIGNMENTS

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RNTSG	S.	œ.—		-	Н	
E	EWRNT	ATTASI	ATTASIR	LSGHRMA	LSGHRMA	
PAASL	PAASL	VKYVG	VKYVG	LYPGH	LYPGH	
LALFSCLIH	LALFSCLIHI	WTPVTPTVA	WTPVTPTVA	QTVQTCNCS1	QTVQTCNCS)	
SFSIFL	SFSIFL	GNTSTC	GNTSTC	FRPRRH	FRPRRH	
FATGNLPGC	FATGNLPGC	PGCIPCVQD	PGCIPCVÓD	VFLVGQAFT	VFLVGQAFT	
ALEDGIN	ALEDGIN	DVILHT	DOVILHT	VGDMCGA'	VGDMCGA	
ALAHGVR	ALAHGVR	SSIVYEA	SSIVYEA	TMCSALY	TMCSALY	
APVGGVAR	APVGGVAR	VLTNDCSN	VLTNDCSN	VDLLVGAA	VDLLVGAA	
1 VG	ı vG	61 LY	61 LY	21 SH	.21 SH	
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PCC1303 penome polyprotein core/El region (isolate HD10-2) - hepatitis C virus (strain type 3) (i C;Species: hepatitis C virus	RESULT 2									
genome polyprotein core/E1 region (isolate HD10-2) - hepatitis C virus (strain type 3) (i C,Species: hepatitis C virus	PC1303									
C, Species: hepatitis C virus	genome polyprotein core/E	1 region	(isolate	HD10-2)	4	epatitis	C virus	(strain	type	=======================================
	C; Species: hepatitis C vi	rus					•			,

Cidate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
Cidate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
Cidatesion: PC1303
Risturyer, L.: Van Arnhem, W.; Myseur, A.; DeLeys, R.; Maertens, G.
Biochem. Blophys. Res. Commun. 192, 635-641, 1993
A.; Hitle: Analysis of the putative B1 envelope and NS4a epitope regions of HCV type 3.
A.; Reference number: PC1303
A.; Reference number: PC1303
A.; Residues: L. 180
A.; Residues: 1-180
A.; Residues: L. 180
A.; Residues: L.

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A; Molecule type: mRNA
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C,Species: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C,Accesion: PC1305
R,Stuyver, L.; Van Arnhem, W.; Myseur, A.; DeLeys, R.; Maertens, G.
Blochem. Blophys. Res. Commun. 192, 635-641, 1993
A,Title: Analysis of the putative El envelope and NS4a epitope regions of HCV type 3.
A,Reference number: PC1300; MUID:93249436; PMID:7683463
A,Rocesion: PC1305
A,Molecule type: MRNA
A,Residues: 1-180 <STU>
A,Residues: 1-180 <STU>
A,Crossion: VNIPROT:QB1277; DDBJ:D14596; NID:g303576; PIDN:BAA03445.1; PID:g3035
A,Cross references: blood
C;Superfamily: hepatitis C virus genome polyprotein
C;Reywords: capsid protein; envelope protein; glycoprotein; transmembrane F;53-64,74-84,91-103,109-118,155-164/Region: hypervariable region #status predicted
F;23-64,74-84,91-103,109-118,155-164/Region: hypervariable region #status predicted
F;25-70,95,166/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: capsid protein; core protein; envelope protein; nonstructural protein; polyp
R; 11-191/Product: core protein #status predicted <COR>
F; 192-372/Product: envelope protein #status predicted <ENV>
F; 373-492/Product: NSI protein (fragment) #status predicted <NSI>
A, Experimental source: blood
C; Superfamily: hepatitis C virus genome polyprotein
C; Kéywords: capsid protein; envelope protein; glycoprotein; polyprotein; transmembrane
F; 55-64, 74-84, 91-103, 109-118, 155-164/Region: hypervariable region #status predicted
F; 52-154/Domain: transmembrane #status predicted <TMM>
F; 57, 70, 95, 166/Binding site: carbohydrate (Asn) (covalent) #status predicted
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NyContains: core protein; envelope protein; NS1 protein
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 06-dan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S41288
R;Seelig, R.
R;Seelig, R.
A;Reference number: S41288
A;Reference number: S4128
A;Reference number: S4128
A;Reference number: S4128
A;Reference number: S4128
A;Residues: 1-492 <SEE>
A;Residues: 1-492 <SEE>
A;Residues: 1-492 <SEE>
A;Cross-references: UNIPROT: Q68870; EMBL:X76918
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100.0%; Pred. No. 3.9e-81;
live 0; Mismatches 0;
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Matches 87; Conserv
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A; Molecule type: mRNA
A; Residues: 1-411 < Liu>A; Molecule type: mRNA
A; Residues: 1-411 < Liu>A; Cross-reterences: UNIPROT: Q81813; GB: L12355; NID: g410169; PIDN: AAA20155.1; PID: g410170
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; F; 192-a83/Product: envelope protein E2/Retus predicted < SPE>
F; 192-433/Product: envelope protein E2/RSI #status predicted < NPE>
F; 196, 209, 234, 305, 325/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Residues: 1.411 CLIJ>
A,Cross-references: UNIPROT:081489
C; Cross-references: UNIPROT:081489
C; Reywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; C; Reywords: ATP; capsid protein = 1 #status predicted < SPB-P
F; 192-383 Product: envelope protein E1 #status predicted < SPB-P
F; 364-411, Product: nonstructural protein E2/NS1 #status predicted < NPE-P; 364-313,305,325/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N; Contains: envelope protein E1; nonstructural protein E2/NS1
C; Species: hepatitis C virus
C; Sate: 14-4/ul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C; Accession: PC2061
R; Li, J.S.; Vitvitski, L.; Tong, S.P.; Trepo, C.
Biochem. Biophys. Res. Commun. 199, 1474-1481, 1994
A; Title: Identification of the third major genotype of hepatitis C virus in France. A; Reference number: PC2066; MUID:94197744; PMID:8147893
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                                                                                                                                                                                                                            111 YVGATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRFRRHQTVQTCNCSLY 170
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C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 14-V10-1994 #sequence_revision 14-V10-1994 #text_change 09-Jul-2004
C;Accession: PC2060
R;Li, J.S.; Vitvitski, L.; Tong, S.P.; Trapp, C.
Biochem. Biophys. Res. Commun. 199, 1474-1481, 1994
A;Title: Identification of the third major genotype of hepatitis C virus in A;Reference number: PC2060; MUID:94197744; PMID:8147893
                                                                                                                                                             111 YVGATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLY
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    Length 180;
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Query Match
38.9%; Score 70; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 4.9e-64;
Matches 70; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.7%; Score 66; DB 2; Le
100.0%; Pred. No. 1.3e-59;
ive 0; Mismatches 0;
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Matches 66; Conservative
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C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C;Accession: PS0165
R;Hijikata, M.; Kato, N.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Shimotohno, K. Biochem. Biophys. Res. Commun. 175, 220-228, 1991
Biochem. Biophys. Res. Commun. 175, 220-228, 1991
A;Title: Hypervariable regions in the putative glycoprotein of hepatitis C virus. A;Reference number: PN0011; MUID:91151353; PMID:1847805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
9.4%; Score 17; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
9.4%; Score 17; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
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Niconcains: capsid procein C; envelope procein M; hepacivirin (EC 3.4.21.98) (nonstructural procein Msda; nonstructural procein Msda; Nicola Msdawa, Nicola Msdawa, S.; Sugiyama, Y.; Kurai, K.; Iizuka, H.; Machida, A.; Miyakawa, Y. G. Gen. Virol. 72, 2697-2704, 1991.

A.Title: Nucleotide sequence of the promore RNA of hepatitis C virus isolated from a hum A; McGenne number: UG1303; NUID:92044440; PMID:1658196

A.Molecule type: genomic RNA
A.Residues: 1-303 cOKAA
A.Residues: 1-3003 cOKAA
A.Residues: 1-3000
A.Residues: 1-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3'-terminal sequences of the genomic RNA of hepatitis
                                                                                                                                              Unusual Ordusual Strain Job (fragments)
N; Contains: NS5 protein
N; Contains: NS5 protein
N; Contains: NS5 protein
C; Species: hepatitis C virus
C; Species: J2-Pb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C; Accession: JQ0891
R; Okamoto, H.
Submitted to JPID, January 1991
A; Description: The 5'-terminal and 3'-terminal sequences of the genomic RNA Of hA; Reference number: JQ0879
A; Recession: JQ089
A; Recession: JQ089
A; Rocession: JQ089
A; Rocession: JR94 COKAP
A; Ross references: UNIPROT:Q7LZYS
A; Ross references: UNIPROT:Q7LZYS
A; Reperimental source: strain J6
C; Repwords: Dolyprotein
C; Repwords: Dolyprotein
F; S10-874/Product: NS5 protein (fragment) #status predicted <NS5>
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10.6%; Score 19; DB 2; Length 874;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 19; Conservative 0; Mismatches 0; Indels
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Matches 19; Conserv
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Shimotohno, K.

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Query Match 9.4%; Score 17;
Best Local Similarity 100.0%; Pred. No.
Matches 17; Conservative 0; Mismatch
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100.0%; Pre
                                                                                                                                                                      165 ATGNLPGCSFSIFLLAL 181
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Best Local Similarity 100.
Matches 17; Conservative
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PC1284
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S12707
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R;Fuchs, K.; Motz, M.; Schreier, E.; Zachoval, R.; Deinhardt, F.; Roggendorf, M.
Rome 103, 163-169, 1991
A;Title: Characterization of nucleotide sequences from European hepatitis C virus isolat
A;Reference number: JN0265; MUID:91365241; PMID:1653756
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N;Contains: capsid protein; envelope protein
C;Species: hepatitis C virus
C;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S21471
N;Mogam, W.K.
submitted to the EMBL Data Library, April 1992
A;Reference number: S21471
A;Referenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome polyprotein - hepatitis C virus (isolate GM2) (fragments)
N;Contains: amino end of envelope protein M; carboxyl end of capsid protein C; fragment
N;Copecies: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
                                                                                                                                       for
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A/Residues: 1-322 <PUC>
A/Rolecule type: genomic RNA
A/Residues: 1-322 <PUC>
A/Cross-references: UNIPROT:003729; GB:M61717; GB:M61718
A/Cross-references: UNIPROT:003729; GB:M61717; GB:M61718
A/Role: the authors translated the codon ACA for residue 198 as Tyr
C/Seywords: capsid protein; envelope protein; glycoprotein; polyprotein; transmembrane
F/110-178/Product: capsid protein C (fragment) #status predicted <CRN-
F/110-178/Product: envelope protein M (fragment) #status predicted <ERM>
F/153-178/Domain: transmembrane #status predicted <TM1-
F/179-322/Product: major envelope protein B (fragment) #status predicted <ERN-
F/179-322/Product: major envelope protein B (fragment)
F/179-322/Product: major envelope protein B (fragment)
F/179-322/Product SATINA (Covalent)
F/179-322/Product SATINA (Covalent)
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F/179-322/Product SATINA (Covalent)
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A;Molecule type: genomic RNA
A;Residues: 1-315 <HIJ>
A;Cross-references: UNIDFOT:Q00906; GB:D00691
A;Note: the authors translated the codon GAC for residues 27 and 11:
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Reywords: Glycotein, polyprotein
F;280-209/Region: hypervariable 1 #status predicted
F;283-289/Region: hypervariable 2 #status predicted
F;5,18,59,114,134,226,232,239,257/Binding site: carbohydrate (Asn)
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 315;
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100.0%; Pred. No. 2.2e-09;
ve 0; Mismatches 0; Indels
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Pred. No. 2.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 9.4%; Score 17; DB Local Similarity 100.0%; Pred. No. 2.2 hes 17; Conservative 0; Mismatches
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Conservative 0;
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A;Molecule type: genomic RNA
A;Residues: 1.441 <TAK>
A;Cross-treferences: UNIPROT:Q81776; EMBL:D00574; NID:g221656; PIDN:BAA00452.1; PID:g22165
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: genomic RNA
A;Residues: 1-513 <OKA>
A;Cross-references: UNIPROT:081221; GB:D00832; NID:g221513; PIDN:BAA00706.1; PID:g221514
C;Superfamily: hepatitis C virus genome polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                 RiTakeuchi, K.; Kubo, Y.; Boonmar, S.; Watanabe, Y.; Katayama, T.; Choo, Q.L.; Kuo, G.; Nucleic Acids Res. 18, 4626, 1990
A; Title: Nucleotide sequence of core and envelope genes of the hepatitis C virus genome A; Reference number: $12707; MUID:90356432; PMID:2117749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome polyprotein - hepatitis C virus (isolate HC-J4) (fragment)
(Species: hepatitis C virus
(Species: hepatitis C virus
(C)Accession: PC1284
(C)Accession: PC1284
(C)Accession: S. Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda, A; Dhu, J. Exp. Med. 60, 167-177, 1990
(A)ATILE: The S-terminal sequence of the hepatitis C virus genome.

A;Reference number: PC1284; MUID:91013116; PMID:2170712
                                                                                                                                                                                                                                                                                                                                                                        C;Accession: $12707
R;Takeuchi, K.; Kubo, Y.; Boonmar, S.; Watanabe, Y.; Katayama, T.; Choo, Q.L.; Kuo, G.;
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                                                                                                                                                                                                                                                                                   N,Contains: core protein, envelope protein
C,Species: hepatitis C virus
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
   Gaps
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Pred. No. 3.3e-09;
0; Mismatches 0;
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   Mismatches
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17;
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1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
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Best Local Similarity 100.
Matches 180; Conservative
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Sequence 22, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 30, Appl
                                                                                                                       December 1, 2004, 23:48:17; Search time 142 Seconds (without alignments) 452.057 Million cell updates/sec
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                                                                                                                                                                                                          US-09-899-046A-20
180
1 VGAPVGGVARALAHGVRALE......TVQTCNCSLYPGHLSGHRMA 180
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1: \cgn2_6\ptodata/2\pubpaa/USO7_PUBCOMB.pep:*

2: \cgn2_6\ptodata/2\pubpaa/USO7_EW_PUB-pep:*

2: \cgn2_6\ptodata/2\pubpaa/USO6_EWEW_PUB-pep:*

4: \cgn2_6\ptodata/2\pubpaa/USO6_EWEW_PUB-pep:*

5: \cgn2_6\ptodata/2\pubpaa/USO6_EWEW_PUB-pep:*

6: \cgn2_6\ptodata/2\pubpaa/USO8_EWEW_PUB-pep:*

7: \cgn2_6\ptodata/2\pubpaa/USO8_EWEW_PUB-pep:*

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9: \cgn2_6\ptodata/2\pubpaa/USO8_EWEW_PUB-pep:*

10: \cgn2_6\ptodata/2\pubpaa/USO8_EWEW_PUB-pep:*

11: \cgn2_6\ptodata/2\pubpaa/USO9_EWECOMB.pep:*

12: \cgn2_6\ptodata/2\pubpaa/USO9_EWECOMB.pep:*

13: \cgn2_6\ptodata/2\pubpaa/USO9_EWECOMB.pep:*

14: \cgn2_6\ptodata/2\pubpaa/USO9_EWECOMB.pep:*

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16: \cgn2_6\ptodata/2\pubpaa/USO9_EWECOMB.pep:*

16: \cgn2_6\ptodata/2\pubpaa/USO9_EWECOMB.pep:*

17: \cgn2_6\ptodata/2\pubpaa/USO9_EWECOMB.pep:*

18: \cgn2_6\ptodata/2\pubpaa/USO9_EWECOMB.pep:*

19: \cgn2_6\ptodata/2\pubpaa/USO0_EWECOMB.pep:*

10: \cgn2_6\ptodata/2\pubpaa/USO0_EWECOMB.pep:*

10: \cgn2_6\ptodata/2\pubpaa/USO0_EWEWCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-899-046-20
US-09-878-281-22
US-09-873-224-20
US-09-873-224-20
US-09-873-224-20
US-09-899-303-30
US-09-995-808-30
US-09-995-808-30
US-09-995-808-30
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                                                                                  protein search, using sw model
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Sequence 91, Appl Sequence 1209, Appl Sequence 14, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 20, Appl Sequence 24, Appl Sequence 26, Appl Sequence 16, Appl Sequence 27, Appl Sequence 28, Appl Sequence 281, Appl Appl Sequence 281, Appl Appl Sequence 281, Appl Appl Sequence 281, Appl Appl Appl Appl Appl Appl Appl App	C virus rophylaxis and therag 25 (BPO)
US-10-128-587A-91 US-09-899-046-18 US-09-899-046-18 US-09-878-281-14 US-09-878-281-18 US-09-878-281-18 US-09-873-224-18 US-09-873-224-18 US-09-873-224-26 US-09-879-046-26 US-09-879-046-26 US-09-879-046-26 US-09-879-24-26 US-09-878-281-26 US-09-878-281-26 US-09-878-281-26 US-09-878-281-26 US-09-873-224-26 US-09-873-224-26 US-09-873-224-26 US-09-873-224-26 US-09-873-224-26 US-09-873-224-26 US-09-873-224-26 US-09-873-224-26 US-09-873-224-26 US-09-873-224-16 US-09-873-224-16 US-09-873-224-16 US-09-873-224-16 US-09-873-224-16 US-10-685-435-5 US-10-685-435-5 US-10-685-435-5 US-10-685-435-5 US-10-685-435-5 US-10-685-435-5 US-10-685-435-5 US-10-685-435-5 US-10-685-435-5 US-10-685-435-5	ALIGNMENTS 46 ces of hepatitis for diagnosis, p 50. 1.0, Version #1. 9,046
41	Man
0.077777777777777777777777777777777777	T. 1 -899-046-20 uence 20, Application US, Lication No. US200300082. APPLICANT: TITLE OF INVENTION: TITLE OF INVENTION: GOMPUTER READABLE FORM: MEDIUM TYPE: Floppy d COMPUTER: IBM PC comp OPERATING SYSTEM: PC-1 SOFTWARE: Patentin Re- SOFTWARE: Patentin Re- SOFTWARE: Patentin Re- SOFTWARE: PATENTION DATA APPLICATION NUMBER: UF FILING DATE: FRING DATE: FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 180 amino acid TYPE: amino acid TYPE: amino acid TYPE: TYPE: protein
4 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 US-09-096-046-20 Sequence 20, Application Publication No. US2003000 GENERAL INFORMATION: APPLICANT: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SECUENCES: COMPUTER READABLE FORM MEDIUM TYPE: Floppy COMPUTER: IBM FC COPENTIER: IBM FILTING DATE: FILLING DATE: FILLING DATE: INFORMATION FOR SEQ ID NEGRETIARY APPLICATION NUMBER: FILLING DATE: INFORMATION FOR SEQ ID NEGRETIARY COPUNGER: FILLING DATE: TYPE: amino acid TYPE: amino acid TYPE: mino acid TYPE: protein

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Gaps

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100.0%; Score 180; DB 10; Length 180; 100.0%; Pred. No. 1.5e-164; ive 0; Mismatches 0; Indels 0.

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FILING DATE:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acids
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                                 61 LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
                                                                                                                  SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180
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                                                                                       121 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180
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    LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
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                                                                                                                                                                                                                                                                                                                   New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy. 270
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TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
TITLE OF INVENTION: 270
COMPUTER READABLE FORM:
MEDIN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VGAPVGGVARALAHGVRALBDGINFATGNLPGGSFSIFLLALFSCLIHPAASLEWRNTSG
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,046
FILING DATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PENTIN RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/878,281
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 180; DB 10; Best Local Similarity 100.0%; Pred. No. 1.5e-164; Matches 180; Conservative 0; Mismatches 0;
                                                                                                                                                                                                              Sequence 22, Application US/09899046

Sequence 22, Application US/09899046

Publication No. US2003008274A1

GENERAL INFORMATION:
TITLE OF INVENTION: Genotypes for di
NUMBER OF SEQUENCES: 270

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: PatentIn Release #1 0 VV
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; Sequence 20, Application US/09878281
; Publication No. US20030032005A1
; GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HILING DATE:
INFORMATION FOR ESO ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acids
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Sequence 22, Application US/09878281
Sequence 22, Application US/09878281
Publication No. US2030032005A1
GENERAL INFORMATION:
TITLE OF INVENTION: Genotypes for diagnosis, prophylaxis and therapy.
TITLE OF INVENTION: Genotypes for diagnosis, prophylaxis and therapy.
NUMBER OF SEQUENCES: 270
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,281
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
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                                                                                        100.0%; Score 180; DB 10;
100.0%; Pred. No. 1.5e-164;
ative 0; Mismatches 0;
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100.0%; Pred. No. 1.5e-164;
iive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 180; Conservative
                                                                                                               Best Local Similarity 100.
Matches 180; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-878-281-20
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SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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CURRENT APPLICATION DATA:
APPLICATION UNDERS.
APPLICATION NUMBER:
FILING DATE: 05-Jun-2001
CLASSIFICATION: «Unknown>
APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
FILING DATE: «Unknown>
APPLICATION NUMBER: 08/362,455
FILING DATE: «Unknown>
ATORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 00 32 9 241 07 11
TELEPHONE: 00 32 9 241 07 99
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
1:ENGTH: 180 mmino acids
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APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
RANDERSSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BYRNE, THOMAS E. REGISTRATION NUMBER: 32,205
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Sequence 30, Application US/09973025;
Publication No. US20020182706A1
GENERAL INFORMATION:
APPLICANT: MARRIENS, GEERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-873-224-22
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                                                         GENERAL INFORMATION:
APPLICANT: <Unknown>
IITLE OF INVENTION: New sequences of hepatitis C virus
genotypes for diagnosis, prophylaxis and therapy.
NUMBER OF SEQUENCES: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LYVLINDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
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CORRESPONDENCE ADDRESS:
STREET: Industriepark Zwijnaarde 7, box 4
CITY: Ghent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG 60
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STREET: Industriepark Zwijnaarde 7, box 4
CITY: Ghent
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100.0%; Pred. No. 1.5e-164;
tive 0; Mismatches 0;
                                                                                                                                                                                                                        CITY: Ghent
COUNTRY: Belgium
ZIP: B-9052
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTE Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/873,224
FILING DATE: 05-Jun-2001
CLASSIFICATION NUMBER: 08/362,455
FILING DATE: COUNTROWN:
APPLICATION NUMBER: 08/362,455
FILING DATE: UNKNOWN:
APPLICATION NUMBER: 08/362,455
FILING DATE: 00/81362,455
TILING DATE: 00/81362,455
TILING DATE: 00/81362,455
TILING DATE: 100 NUMBER: 08/362,455
TILING DATE: 00/81362,455
TILING DATE: 100 NUMBER: 08/362,455
TILING DATE: 100 NUMBER: 08/362,455
TELEPHONE: 00/82 9 241 07 91
TELEPHONE: 00/82 9 241 07 91
TELEPHONE: SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09873224
Squence 22, Application No. US20030064360A1
GENERAL INFORMATION:
APPLICANT: <Unknown>
             Sequence 20, Application US/09873224
Publication No. US20030064360A1
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ZIP: B-9052
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Best Local Similarity 100.
Matches 180; Conservative
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US-09-873-224-22
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                                                                                       1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
                                                Gaps
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COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC competible
COMPUTER: IBM FC COMPETIBLE
COMPUTER: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/09/973,025
FILING DATE: 10-OCC-2001
CLASSIFCATION: UNKNOWN>
Length 180;
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Query Match
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DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VIRGINIA.
STATE: VIRGINIA.
ZIP: 22201-4714
CONPUTER: EDADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION NUMBER: US/09/899.303
FILING DATE: 06-Jul-2001
CLASSIFICATION: CURKNOWN>
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0
                                                                                                                                                                                                                                                       Length 208;
                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                       Score 180; DB 9; Le,
Pred. No. 1.7e-164;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1487-10
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-973-025-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/09899303 Publication No. US20030036110A1 GENERAL INFORMATION:
                                                                           INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acid
TYPE: amino acid
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                                                          (703) 816-4100
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Best Local Similarity
Matches 180; Conservat
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US-09-995-860-30

US-09-995-860-30

Sequence 30, Application US/09995860

Sequence 30, Application US/09995860

Publication No. US20030118603A1

GENERAL INFORMATION:

TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and TITLE OF INVENTION: Therapeutic use.

FILE REFERENCE: 2551-69

CURRENT APPLICATION NUMBER: US/09/995,860.

CURRENT APPLICATION NOWS: 122

SOFTWARE: PatentIn 3.1

SEQ ID NO 30

SEQ ID NO 30

TYPE: PRT
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Publication No. US20030095980A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
TITLE OF INVENTION: therapeutic use.
FILE REFERENCE: 2551-70
CURRENT APPLICATION NUMBER: US/09/995,808
CURRENT APPLICATION NUMBER: 2001-11-29
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin 3.1
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100.0%; Pred. No. 1.7e-164;
iive 0; Mismatches 0;
                                                                                                 100.0%; Score 180; DB 10;
100.0%; Pred. No. 1.7e-164;
ive 0; Mismatches 0;
MOLECULE TYPE: protein SEQ ID NO: 30: US-09-899-303-30
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Best Local Similarity 100.0%;
Matches 180; Conservative 0
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; ORGANISM: Hepatitis C virus
US-09-995-808-30
                                                                                                                               Best Local Similarity 100.
Matches 180; Conservative
                                                                                                                             Similarity
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US-09-995-808-30
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RESULT 14
US-10-128-587A-91
US-10-128-587A-91
US-10-128-587A-91
Sequence 91, Application US/10128587A
Publication No. US20030152940A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: proteins
TITLE OF INVENTION: proteins
TITLE OF INVENTION: DAY
CURRENT APPLICATION WHMBER: US/10/128,587A
UUMBER OF SEQ ID NOS: 98
UUMBER OF SEQ ID NOS: 98
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; Publication No. US2030108561A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
; FILE REFERENCE: 135 PCT
; CURRENT FILICATION UNSER: US/10/128,590
; CURRENT FILICATION UNSER: 2002-07-22
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
                                                                                                                                                         Length 208;
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                                                                                                                                                         Query Match 100.0%; Score 180; DB 16; Best Local Similarity 100.0%; Pred. No. 1.7e-164; Matches 180; Conservative 0; Mismatches 0;
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; ORGANISM: hepatitis C virus
US-10-128-590-91
                                                   TYPE: PRT
ORGANISM: Hepatitis C virus
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US-10-128-590-91
                                                                                                         US-10-321-798-30
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SEQ ID NO 91
LENGTH: 209
SEQ ID NO 30
LENGTH: 208
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Publication No. US20040126395A1
GENERAL INFORMATION:
TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and TITLE OF INVENTION: therapeutic use.
TITLE OF INVENTION: therapeutic use.
FILE REPERENCE: 2551-93
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/10/321,798
PRIOR APPLICATION NUMBER: 10/020,510
PRIOR PILING DATE: 2002-10-16
PRIOR PILING DATE: 2002-10-16
PRIOR PILING DATE: 2001-10-18
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin 3.1
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US-09-955-791-30
US-09-955-791-30
Sequence 30, Application US/09995791
Publication No. US20030147918A1
GENERAL INFORMATION
TITLE OF INVENTION: Parified hepatitis C virus envelope proteins for diagnostic and
TITLE OF INVENTION: therapeutic use.
TITLE OF INVENTION: therapeutic use.
TITLE OF INVENTION: US/09/995,791
CURRENT APPLICATION NUMBER: US/09/995,791
CURRENT PILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin 3.1
SEQ ID NO 30
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100.0%; Score 180; DB 10; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.7e-164;
Matches 180; Conservative 0; Mismatches 0; Indels 0
                                                                               Length 208;
                                                                                                                                  0; Indels
                                                                            ; Score 180; DB 10;
; Pred. No. 1.7e-164;
0; Mismatches 0;
                                                                            Query Match
Best Local Similarity 100.0%;
Matches 180; Conservative 0;
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; ORGANISM: Hepatitis C virus
US-09-995-791-30
  ; ORGANISM: Hepatitis C virus US-09-995-860-30
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US-10-321-798-30
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Sequence 209, Application US/10651165

Publication No. US200400478771

GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELECYS, Robert
APPLICANT: ON UNMERS: US/10/651,165
FILE REFERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/08/974,690C
PRIOR APPLICATION NUMBER: POT/EP94/03555
PRIOR PILING DATE: 1994-11-19
PRIOR FILING DATE: 1994-11-0-28
PRIOR FILING DATE: 1994-11-0-4
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATOR HUNG DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATOR HUNG DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATOR HUNG DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATOR HUNG DATE: 1993-11-04
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NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATOR HUNG DATE: 1993-11-04
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                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus US-10-128-587A-91
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Best Local Similarity 100.0%; Pred. No. 1.7e-164;
Matches 180; Conservative 0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Pred. No. 5.2e-80;
Matches 92; Conservative 0; Mismatches 0;
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TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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Search completed: December 1, 2004, 23:58:05 Job time : 143 secs 16, Appl 189, Appl 189, Appl 190, Appl 190, Appl 90, Appl 90, Appl 90, Appl 90, Appl 188, Appl 89, Appl 80, App

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RESULT 2
US-09-878-281A-22
US-09-878-281A-22
Sequence 22, Application US/09878281A
Sequence 22, Application US/09878281A
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph)
TITLE OF INVENTION: and therapy
TITLE OF INVENTION: and therapy
TITLE OF INVENTION: and therapy
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
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100.0%; Score 180; DB 4;
Best Local Similarity 100.0%; Pred. No. 2e-165;
Matches 180; Conservative 0; Mismatches 0;
US-09-878-281A-16
US-08-290-665A-187
US-08-290-665A-189
US-08-290-665A-199
US-08-290-665A-199
PCT-US95-10398-189
PCT-US95-10398-190
US-08-466-601A-90
US-08-466-601A-90
US-08-466-601A-90
US-08-290-665A-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09978281A
Patent No. 6762024
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: New sequences of hepatiti:
TITLE OF INVENTION: and therapy
FILE REPERENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 180
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                                             TYPE: PRT ORGANISM: hepatitis C virus
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US-09-878-281A-14
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APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYES, MARTYNOFF, GUY
APPLICANT: BUYES, MARTYNOFF, GUY
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROPIENS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 1487-10
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPAK: (703) 816-4100
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
TENGTH: 208 amino acids
                                                                                                                                                           Indels
                                                                                                          ; Score 180; DB 4;
; Pred. No. 2e-165;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/08612973; Patent No. 6150134; GENERAL INFORMATION:
                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 180; Conservative 0
; LENGTH: 180
; TYBE: PRT
; ORGANISM: hepatitis C virus
US-09-878-281A-22
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MOLECULE TYPE: protein
US-08-612-973-30
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Best Local Similarity
Matches 180; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LYVLINDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MARKTENS, GERRT
APPLICANT: BOSNAN, FONS
TITLE OF INVENTION: PROTEINS FOR DIAGN
TITLE OF INVENTION: PROTEINS FOR DIAGN
NUMBER OF SEQUENCES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COMPUTE: VIRGINIA
COMPUTER: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
COMPUTER: ISM PC COMPACIBLE
COMPUTER: ISM PC COMPACIBLE
COMPUTER: ISM PC COMPACIBLE
COMPUTER: ISM PC COMPACIBLE
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APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOWAS E.
REGISTATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     Sequence 30, Application US/08927597
Patent No. 6245503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-927-597-30
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Sequence 209, Application US/08974690C

Sequence 209, Application US/08974690C

Sequence 209, Application US/08974690C

GENERAL INFORMATION:

APPLICANT: LEROUX-ROELS, Geert

APPLICANT: MAERTENS, Geert

APPLICANT: MAERTENS, Geert

APPLICANT: MAERTENS, Geort

APPLICANT: MAERTENS, Geort

APPLICANT: MAERTENS, Geort

CURRENT APPLICATION NUMBER: US/08/974,690C

CURRENT APPLICATION NUMBER: P07/EP94/03555

PRIOR PALING DATE: 1994-11-19

PRIOR PALING DATE: 1994-11-04

NUMBER OF SEQ ID NOS: 286

SEQ ID NOS: 286

SEQ ID NO 209

LENGTH: 187

LENGTH: 187
         Sequence 209, Application US/08635886C
Patent No. 655514
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: INMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VRUS
TITLE OF INVENTION: VRUS
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT APPLICATION NUMBER: P20/EP94/03555
PRIOR PAPLICATION NUMBER: EP 93402718.6
PRIOR PILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1930-11-04
NUMBER OF SEQ ID NOS: 286
SSOCIED NO 209
LENGTH: 187
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1e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 GOAFTFRPRRHOTVQTCNCSLYPGHLSGHRMA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 GQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
51.1%; Score 92; DB
Best Local Similarity 100.0%; Pred. No. 1e-
Matches 92; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 ) TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-209
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, ORGANISM: hepatitis C virus
US-08-974-690C-209
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US-08-974-690C-209
US-08-635-886C-209
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Squence 1... Application US/09878281A

Patent No. 6762024

GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: and therapy

TITLE OF INVENTION: and therapy

TITLE OF INVENTION: MARK: US/09/878,281A

CURRENT APPLICATION NUMBER: US/09/878,281A

CURRENT PILING DATE: 2001-06-12

NUMBER OF SEQ ID NOS: 284

SOFTWARE: Patentin version 3.1

SEQ ID NO 14

SEQ ID NO 14

SEQ ID NO 14
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Sequence 18, Application US/09878281A

GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: and therapy

TITLE OF INVENTION: and therapy

TITLE OF INVENTION: and therapy

CURRENT APPLICATION NUMBER: US/09/878,281A

CURRENT APPLICATION NUMBER: US/09/878,281A

NUMBER OF SEQ ID NOS: 284

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 204
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Best Local Similarity 100.0%; Pred. No. 6.4e-76;
Matches 87; Conservative 0; Mismatches 0; Indels
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48.3%; Score 87; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.4e-76;
Matches 87; Conservative 0; Mismatches 0; Indels
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Sequence 207, Application US/08635886C
Patent No. 6555114
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-09-878-281A-18
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: hepatitis C virus
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JS-09-878-281A-14
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GENERAL INFORMATION:
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LENGTH: 193
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Sequence 207, Application US/08974690C

PATENT NOTE OF APPLICANT: LEROWY ROLES, Geart
APPLICANT: LEROWY ROLES, Geart
APPLICANT: MAERTENS, Geart
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/08/974,690C
CURRENT APPLICATION NUMBER: DCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR APPLICATION NUMBER: DCT/EP94/03555
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APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
fITLE OF INVENTION: VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 187;
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                                                                                    THIER REPERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: EP 94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
LENGTH: 187
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Matches 87; Conserv
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Best Local Similarity
Matches 87; Conserv
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US-08-635-886C-210
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US-08-974-690C-207
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US-08-974-690C-210

US-08-974-690C-210

Sequence 210, Application US/08974690C

Sequence 210, Application US/08974690C

SENERAL INFORMATION:
APPLICANT: LELEWAYION:
APPLICANT: DELEYS, ROBERT

APPLICANT: MARKTENS, Geert

APPLICANT: MARKTENS, Geert

TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: VIRUS

FILE REFREENCE: 2551-94

CURRENT APPLICATION WUMBER: US/08/974,690C

CURRENT FILING DATE: 1997-11-19

PRIOR APPLICATION WUMBER: EP 93402718.6

PRIOR PRIOR DATE: 1993-11-04

NUMBER OF SEQ ID NOS: 286

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 210

TENAMENT: PATENTIN VERSION 3.1
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APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEVE, Robert
APPLICANT: DELEVE, Robert
APPLICANT: MAERTENS, Geert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: URRUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: URRUNS
TITLE OF INVENTION: VARUS
TITLE OF INVENTION UNMER: US/08/635,886C
CURRENT APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-11-04
PRIOR FILING DATE: 1994-11-04
PRIOR FILING DATE: 1994-11-04
NUMBER OF SEQ ID NOS: 286
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48.3%; Score 87; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.8e-76;
Matches 87; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 6.8e-76;
Matches 87; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: hepatitis C virus
US-08-635-886C-210
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US-08-974-690C-210
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RESULT 13

; Sequence 210, Application US/08635886C; Patent No. 6555114

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Gaps ; 0

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111 YVGATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLY
                                                                                                                                                                                                                                            Query Match
38.9%; Score 70; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 70; Conservative 0; Mismatches 0; Indels
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  CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ 1D NOS: 284
SOFTWARE: Patentin version 3.1
SEQ 1D NO 28
LENGTH: 180
TYPE: PRT
CRGANISM: hepatitis C virus
US-09-878-281A-28
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US-09-878-281A-24

Sequence 24, Application US/09878281A

Sequence 24, Application US/09878281A

Sequence 24, Application US/09878281A

GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: and therapy

FILE REFRENCE: 35

CURRENT APPLICATION NUMBER: US/09/878,281A

CURRENT APPLICATION NUMBER: US/09/878,281A

CURRENT APPLICATION NUMBER: US/09/878,281A

SOUTHWARE: PATENTING DATE: 2001-06-12

NUMBER OF SEQ ID NOS: 284

SEQ ID NO 24

LENGTH: 180

TITLE: PRT

TITLE: THE PRESENCE: SEQ ID NOS: 284

SEQ ID NO 24

LENGTH: 180

TITLE: PRT

TITLE: THE PRESENCE: SEQ ID NOS: 284

SEQ ID NO 24

LENGTH: 180

TITLE: THE SEC ID NOS: 284

SEQ ID NO 24

LENGTH: 180

TITLE: THE SEC ID NOS: 284

SEQ ID NOS 24

LENGTH: 180

TITLE: THE SEC ID NOS: 284

SEQ ID NOS 24

LENGTH: 180

TITLE: THE SEC ID NOS: 284

LENGTH: 180
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Patent No. 6762024
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
TITLE OF INVENTION: and therapy
TITLE OF INVENTION: and therapy
TITLE OF INVENTION: 31
SEQ ID NO 26
LENGTH: 180
TYPE: PRT
CORRENT APPELIES
TORGHISM: hepatitis C virus
US-09-878-281A-26
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Patent No. 6762024
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
TITLE OF INVENTION: and therapy
FILE REFERENCE: 35
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Pred. No. 1.5e-59;
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100.0%; Pred. No. ...
0; Mismatches
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38.9%; Score 70; DB
Best Local Similarity 100.0%; Pred. No. 1.5
Matches 70; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 70; Conservative
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US-09-878-281A-28
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US-09-878-281A-26
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MEDLINE-93249436; PubMed=7683463;

A Stuyer L., Arnhem W.V., Wyseur A., Deleys R., Maertens G.;

Stuyer L., Arnhem W.V., Wyseur A., Deleys R., Maertens G.;

Stuyer L., Arnhem W.V., Wyseur A., Deleys R., Maertens G.;

Stuyer L., Arnhem W.V., Wyseur A., Deleys R., Maertens G.;

T type 3.";

B iochem. Blophys. Res. Commun. 192:635-641(1993).

R BMBL, D14599; BAA03448...;

R BMBL, D14599; BAA03448...;

R GO; GO:0016021; C:initegral to membrane; IEA.

GO; GO:0019029; C:viral capaid; IEA.

GO; GO:001901; C:viral envelope; IEA.

GO; GO:0005199; F:structural molecule activity; IEA.

InterPro; IPR002521; HCV_core.

R InterPro; IPR002521; HCV_core.

R Pfam; PF01542; HCV_core.

R Pfam; PF01542; HCV_core, 1.

R Pfam; PF01539; HCV_core, 1.

R Can protein; Envelope protein; Glycoprotein; Polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=core-E1;
Hepatitis C virus.
Virusės; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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100.0%; Score 964; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.2e-86;
Matches 180; Conservative 0; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Core protein-envelope 1 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 AA
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      06X741
06X744
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068801
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            пиприприприпри
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            Hepacivirus.
NCBI_TaxID=11103;
         Transmembrane.
NON TER 1
NON TER 180
SEQUENCE 180
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(without alignments)
536.619 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                     .....TVQTCNCSLYPGHLSGHRMA 180
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                                     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                           - protein search, using sw model
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2: uniprot_trembl:*
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Gapop 10.0 , Gapext
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length: 2000000000
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Maximum DB
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Gaps

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Seelig R., Weber P., Seeling H.P., Ledger N., Bottner C., Renz M., Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                 GO: GO: 0016011, G: integral to membrane; IEA.
GO: 00109128; C: viral capsid; IEA.
GO: GO: 0010524; E: AIP binding; IEA.
GO: GO: 0008524; E: AIP binding; IEA.
GO: GO: 0008528; E: AIP bending; IEA.
GO: GO: 000858; E: AIP binding; IEA.
GO: GO: 000858; E: RNA-directed RNA polymerase activity; IEA.
GO: GO: 000858; E: RNA-directed RNA polymerase activity; IEA.
GO: GO: 000858; E: Serine-type peptidase activity; IEA.
GO: GO: 000858; E: Serine-type peptidase activity; IEA.
GO: GO: 000858; F: Serine-type peptidase activity; IEA.
GO: GO: 0006508; F: Protecolysis and peptidolysis; IEA.
GO: GO: 0006508; P: priral genome replication; IEA.
GO: GO: 0019979; P: viral genome replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3021;
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NS4a protein.
NS4a protein.
Core protein.
NS5b protein.
NS5b protein.
NS5b protein.
NS5b protein.
NS1 protein.
NN1 protein.
NN1 protein.
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99.6%; Score 960; DB 2; Length 30
Best Local Similarity 98.9%; Pred. No. 1.2e-84;
Matches 178; Conservative 2; Mismatches 0; Indels
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IPR002518; Pept_U39_HCV N
IPR007095; RNA_pol_DS_PS_
IPR007094; RNA_pol_PSvir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000345; CytC heme_BS IPR001410; DEAD.
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IPR0025119; HCV NS1...
IPR000745; HCV NS48...
IPR000745; HCV NS48...
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                                                                                                                   EMBL; X76918; CAA54244.1;
                                                                                                                                    PIR; PC1307; PC1307.
PIR; PC0401; PC0401.
PIR; PC0804; PC0804.
PIR; S41288; S41288.
HSSP; P27958; 1A1V.
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384 73
3021 AA;
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                                       SEQUENCE FROM N.A.
    NCBI_TaxID=11103;
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=94065664; PubMed=7504073;
Okamoto H., Tokita H., Sakamoto M., Horikita M., Kojima M., Iizuka H.,
Mishiro S.;
                                                                                                                                                                                                                                                                                                                 "Characterization of the genomic sequence of type V (or 3a) hepatitis C virus isolates and PCR primers for specific detection."; J. Gen. Virol. 74:2385-2390(1993).
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Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01554; HCV_core; 1.
Pfam; PF01559; HCV_env, 1.
Pfam; PF01560; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; CHAIN
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Genes for core, envelope and NS1 proteins.
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Pred. No. 1.7e-85;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Okamoto H.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
EMBL: D14105; BAA03251.1; -.
PIR; PQ0804; PQ0804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GG; GC:0016021; C:integral to membrane, IEA.
GG; GC:0019028; C:viral capsid; IEA.
GG; GC:0019031; C:viral capsid; IEA.
GG; GC:0019031; C:viral capsid; IEA.
GG; GC:0005198; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_env.
                                                                                  Last sequence update)
Last annotation update)
                         503 AA.
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E.
E2/NS1.
                                                               Created)
                         PRT;
Q81752
ID Q81752
DT 081752;
DT 01-NOV-1996 (TrEMBLrel. 01, Cr
DT 01-NOV-1996 (TrEMBLrel. 01, La
DT 01-OCT-2003 (TrEMBLrel. 25, La
DE POlyprotein (Fragment).
OS Hepatitis C virus
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Best Local Similarity 98.9°
Matches 178; Conservative
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SEQUENCE FROM N.A.
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AC Q66
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                                                                             SHVDLLVGAATMCSALYVGDMCGAVFLVQQAFTFRPRHQTVQTCNCSLYPGHLSGHRMA 319
 LYVLTNDCSNSSIVYBADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
                                                       121 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180
                                                                                                                                                      Q81258 PRELIMINARY; PRT; 3021 AA.
Q81258;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein.
Hepatitis C virus.
Hepatitis C virus.
Hepatitis C virus.
Hepatitis T virus.
Hepatitis C virus.
Hepatitis T virus.
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IS SUCCESSED.

SUBMITTEE (SEP193) to the EMBL/GenBank/DDBJ databases.

EMBL: D17763; BAA046609.1; -. SEP16010.1; D176010.1; D1760
                                                                                                                                                                                                                                                                                                                                     Sakamoto M.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
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| R | PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1. | R | PROSITE; PS00415; PERCOXIDASE 1; UNKNOWN_1. | R | COAITE; PS00415; PERCOXIDASE 1; UNKNOWN 1. | COAITE; PS00415; PERCOXIDASE 1; UNKNOWN 1. | COAITE; PS004015; PS0
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TISSUE=Serum;
MEDILINE=91156678; PubMed=1705704;
Han J.H., Shyamala V., Richman K.H., Brauer M.J., Tekamp-Olson P.;
"Characterization of the terminal regions of hepatitis C viral RNA:
Identification of conserved sequences in the 5'-untranslated region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Naturctural region (Fragment).
Name=structural region;
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Li J.S., Vitvitski L., Tong S.P., Trepo C.;
"Identification of the third major genotype of hepatitis C virus
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TISSUB-Serum;

MEDLINE=91172826; PubMed=1848704;

Choo Q., Richman K.H., Han J.H., Berger K., Lee C., Dong C.,

Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J.,

Bradley D.W., Kuo G., Houghton M.;

"Genetic organization and diversity of the hepatitis C virus.";

Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455(1991).
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Pred. No. 1.2e-84;
2; Mismatches 0; Indels
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EMBL, L12355; AAA20155.1; -.
PIR; PC2061; PC2061.
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Matches 178; Conservative
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TISSUE=Serum;
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NCBI_TaxID=11103;
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61 LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
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Hepacivirus.
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MEDLINE=93249436; PubMed=7683463;
MEDLINE=93249436; PubMed=7683463;
MEDLINE=93249436; PubMed=7683463;
Stuyver L., Arnhem W.V., Wyseur A., Deleys R., Maertens G.;
Stuyver L., Arnhem W.V., Wyseur A., Deleys R., Maertens G.;
Type 3.",
Expe 3.",
Blochem. Biophys. Res. Commun. 192:635-641(1993).
PIR; PC1303; PC1303.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019023; C:viral envelope; IEA.
GO; GO:001918; F:structural molecule activity; IEA.
InterPro; IPR002521; HCV_core.
Pfam; PF01542; HCV_core.
Pfam; PF01539; HCV_core; 1.
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X Stuyver L., Arnhem W.V., Myseur A., Deleys R., Maertens G.;

A Stuyver L., Arnhem W.V., Myseur A., Deleys R., Maertens G.;

Stuyver L., Arnhem W.V., Myseur A., Deleys R., Maertens G.;

Type 3."; in the putative El envelope and NS4a epitope region of HCV

I shochem. Biophys. Res. Commun. 192:635-641(1993).

B Biochem. Biophys. Res. Commun. 192:635-641(1993).

R Biochem. Biophys. Res. Commun. 192:635-641(1993).

R GO; GO:0019023; Colinegral to membrane; IEA.

GO; GO:0019023; Colinegral to membrane; IEA.

GO; GO:0019031; Colinegral capsid; IEA.

GO; GO:0019028; F:structural molecule activity; IEA.

R InterPro; IPR002519; HCV core.

R InterPro; IPR002519; HCV core.

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R Pfam; PF01539; HCV core; I.
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R GO; GO:0019028; C:viral capsid; IEA.
R GO; GO:0019021; C:viral capsid; IEA.
R GO; GO:0005198; E:structural molecule activity; IEA.
R InterPro; IPR00252; HCV_core.
R InterPro; IPR002521; HCV_core.
R InterPro; IPR002519; HCV_core.
R InterPro; IPR002519; HCV_core.
R Pfam; PF01543; HCV_core; 1.
R Pfam; PF01539; HCV_core; 1.
R Pfam; PF01549; HCV_core; 1.
R Pfam; PF01540; HCV_core
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Core protein-envelope 1 protein (Fragment).
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GO; GO: 0019028; C: viral capsid; IEA.

GO; GO: 0019028; C: viral capsid; IEA.

GO; GO: 0019028; C: viral capsid; IEA.

RO; GO: 0019028; C: viral capsid; IEA.

RO; GO: 0019028; C: viral capsid; IEA.

RO; GO: 0019028; F: structural molecule activity; IEA.

InterPro; IPR002521; HCV capsid.

RITERPO; IPR002521; HCV capsid.

RITERPO; IPR002519; HCV capsid.

RITERPO; IPR0143; HCV capsid; I.

REAM; PF01542; HCV capsid; I.

REAM; PF01540; HCV corv; I.

REAM; PF01560; HCV NS1; I.

ROat protein; Transmemperane.

THAIN CHAIN: Transmemperane.

THAIN CHAIN: Transmemperane.

THAIN CAPSIDE TRANSMEMBER TO C.

THA
                                                                                                                                                                                          MEDLINE=94065664; PubMed=7504073;
Okamoto H., Tokita H., Sakamoto M., Horikita M., Kojima M., Iizuka H.,
Mishiro S.;
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MEDLINE=94065664; PubMed=7504073;
Okamoto H., Tokita H., Sakamoto M., Horikita M., Kojima M., Iizuka H.,
Mishiro S.;
                                                                                                                                                                                                                                                                                                                     hepatitis
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Hepadivirus.
NCBI_TaxID=11103;
                                     .ruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                                                                                                                                          "Characterization of the genomic sequence of type V (or 3a) C virus isolates and PCR primers for specific detection."; J. Gen. Virol. 74:2385-2390(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okamoto H.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; D14311; BAA03257.1; -
PIR; PC2066) PC2066.
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>503 E2/NS1.
503 WW, 2FE38EC30F779229 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, C.
01-NOV-1996 (TrEMBLrel. 01, L.
01-OCT-2003 (TrEMBLrel. 25, L.
Polyprotein (Fragment).
Hepatitis C virus.
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384 >5
503 5
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nes 175; Conserv
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                                                                                                NCBI_TaxID=11103;
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140 VGAPVGGVARALAHGVRALEDGINFATGNLFGCSFSIFLLALLSCLIHPAASLEWRNTSG 199
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DR FMBL, D14309; BA403255.1; -.

PR FIR, PQ0804; PQ0804; PQ0804.

PIR, PQ0804; PQ0804; PQ0804.

DR GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:iviral capsid, IEA.

DR GO; GO:0019031; C:viral enclope; IEA.

GO; GO:0019031; C:viral enclope; IEA.

DR GO; GO:0019031; C:viral enclope; IEA.

DR GO; GO:005199; F:structural molecule activity; IEA.

DR InterPro; IPR002521; HCV_core.

DR InterPro; IPR002531; HCV_core.

DR InterPro; IPR002531; HCV_core.

DR InterPro; IPR002531; HCV_env.

DR Ffam; PF01543; HCV_core; 1.

R Ffam; PF01543; HCV_env; 1.

R Ffam; PF01543; HCV_env; 1.

R Ffam; PF01540; HCV_NS1; 1.

R Ffam; PF01560; HCV_NS1; 1.

R Ffam; PF01560; HCV_NS1; 1.

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Hepatitis C virus.
Viruses; sRRNA positive-strand viruses, no DNA stage; Flaviviridae;
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GO:0019028; C:viral capsid; IEA.
GO:0019031; C:viral careloge, IEA.
GO:000524; F:ATP anding; IEA.
GO:0003723; F:RTA binding; IEA.
GO:0003723; F:RTA binding; IEA.
GO:0003788; F:RTA binding; IEA.
GO:0003286; F:serine-type peptidase activity; IEA.
GO:0008286; F:serine-type peptidase activity; IEA.
GO:0008286; F:serine-type peptidase activity; IEA.
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Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
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E.
E2/NS1.
Gen. Virol. 74:2385-2390(1993).
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Best Local Similarity 97.8%;
Matches 176; Conservative
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C virus isolates and PCR primers for specific detection.";

Hepatitis C virus.

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Matches 173; Conservative
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                                                                                                                                                                                                                                             Similarity
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepacivirus.
NCBI_TaxID=11103;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                    Query Match
Best Local
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Q81495;
                                                                                                                                                                                               CHAIN
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DORRADORRAN
SFTT FFT SO
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-94065664; PubMed-7504073;
Okamoto H., Tokita H., Sakamoto M., Horikita M., Kojima M., Iizuka H.,
Mishiro S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of the genomic sequence of type V (or 3a) hepatitis C virus isolates and PCR primers for specific detection.", J. Gen. Virol. 74:2385-2390(1993).
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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97.2%; Pred. No. 6.7e-83;
tive 3; Mismatches 2; Indels
GO; GO:0006508; P:proteolysis and peptidolysis; IBA. 60; CO:0006530; P:transcription; IBA. 60; GO:0019079; P:viral genome replication; IBA. 60; GO:0019087; P:viral transformation; IBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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                                                                                                                                        InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR002518; Pept U39 HCV NS2.
InterPro; IPR007095; RNA pol DS PS.
InterPro; IPR0070994; RNA pol PSVir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                               Peptidase S29.
                                      InterPro; IPR000345; CytC_heme_BS
InterPro; IPR001410; DEAD.
                                                               Interpro; IPR002521; HCV_core.
Interpro; IPR002519; HCV_env.
Interpro; IPR002531; HCV_NS43.
Interpro; IPR00149; HCV_NS44.
Interpro; IPR001499; HCV_NS45.
Interpro; IPR001868; HCV_NS53.
Interpro; IPR002166; HCV_RGRP.
Interpro; IPR004109; PebFidase.
                                                       InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV core.
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 97.23
Matches 175; Conservative
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Hepatitis C virus.
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200 LYILINDCSNSSIVYEADDVILHTPGCIPCVHNGNTSTCWTPVTPTVAVRHVGATASIR 259
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                                                                   1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSPSIFILLALFSCLIHPAASLEWRNTSG 60
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STRANBKAB,
MEDLINE-55053917; PubMed=7964640;
Yamada N., Manihara K., Mizokami M., Obba K., Takada A., Tsutsumi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Heparitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage, Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Full-length sequence of the genome of hepatitis C virus type 3a: comparative study with different genotypes."; Gen. Virol. 75.3279-3284(1994).
EMBL; D28917; BAA06044.1; -
HSSP; P27958; IHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO: 0016021; C:integral to membrane; IEA.
GO; GO: 0019021; C:viral capsid; IEA.
GO; GO: 0019031; C:viral envelope; IEA.
GO; GO: 0005524; F:APP binding; IEA.
GO; GO: 0003723; F:RNA binding; IEA.
GO; GO: 0003723; F:RNA binding; IEA.
GO; GO: 0003768; F:RNA dinding; IEA.
GO; GO: 0003868; F:RNA-dependent helicase activity; IEA.
GO; GO: 0003788; F:RNA-dependent helicase activity; IEA.
GO; GO: 0008236; F:RNA-dependent helicase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.0%; Score 935; DB 2; Length 50 96.1%; Pred. No. 4.7e-83; Antive. 5; Mismatches 2; Indels
Okamoto H.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
EMBL: D14307; BAA03253.1; -.
PIR; PQ0804; PQ0804.
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503 AA; 54900 MW; E37704D2A438A828 CRC64;
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Last sequence update)
Last annotation update)
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E.
E2/NS1.
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us-09-899-046a-20.rup

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

GO; GO:0019079; P:viral geneme replication; IEA.

GO; GO:0019079; P:viral geneme replication; IEA.

InterPro; IPR001401 DEAD.

InterPro; IPR001401 DEAD.

InterPro; IPR002521; HCV_core.

InterPro; IPR002521; HCV_core.

InterPro; IPR002531; HCV_NS1.

InterPro; IPR001490; HCV_NS4.

InterPro; IPR001490; HCV_NS4.

InterPro; IPR001400; Peptidase S29.

InterPro; IPR0000003; Peptidase S29.

InterPro; IPR0000004; Peptidase S29.

InterPro; IPR00000004; Peptidase S29.

InterPro; IPR00000004; Peptidase S29.

InterPro; IPR00000004; IRV_NS2; II.

IPR MM; PF001560; HCV_NS2; II.

IPR MM; PF001560; HCV_NS49; II.

IPR MM; PF00106; HCV_NS49; 3021 AA; 328387 MW; A97418FF36C062A4 CRC64; Query Match

96.8%; Score 933; DB 2;
Best Local Similarity 96.1%; Pred. No. 5.1e-82;
Matches 173; Conservative 3; Mismatches 4; SEQUENCE

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Gaps

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4; Indels

SEQUENCE FROM N.A.
MEDLINE=9201770; PubMed=8151307;
TCKita H., Shrestha S.M., Okamoto H., Sakamoto M., Horikita M.,
Iizuka H., Shrestha S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Nepal with novel genotypes and their classification into the third major group.";
U. Gen. Virol. 75:931-936(1994). 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Core, env, and part of E2/NS1 (Fragment).
Hepatitis C virus.
Hepatitis C virus.
Hepatitis C virus. 415 AA PRELIMINARY; NCBI_TaxID=11103; RESULT 13 Q81546

121 SHVDLIVGAATMCSALYVGDWCGAVFLVGQAFTRPRRHQTVQTCNCSLYPGHLSGHRMA 180 199 260 GHVDLLVGTATLCSALYVGDLCGAVFLVGQAFTFRPRRHQTVQHCNCSLYPGHVSGHRMA 319 61 LYVLTNDCSNSSIVYBADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120 REDINE=94186155; PubMed=8138250;

A SECURNE=94186155; PubMed=8138250;

A Shreetha S.M., Tsuda F., Okamoto H., Tokita H., Horikita M.,

A Tanaka T., Miyakawa Y., Mayumi M.;

A Tanaka T., Miyakawa Y., Mayumi M.;

Tanaka J., Miyakawa Y., Mayumi M.;

Tanaka J., Banaka J., Mayumi M.;

Tanaka J., Miyakawa Y., Mayumi M.;

Tanaka J., Miyaka J., Miyaka J., Miyaka J., Miyaka Mayaka J., Mayaka Mayaka J., Mayaka Mayaka J., Mayaka 9 200 LYILTNDCSNSSIVYEADHVILHLPGCVPCVQNNNTTTCWIPVTPTVAVSHVGATTASIR 1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG 0; Gaps Length 415; 11; Indels Query Match 89.7%; Score 865; DB 2; Best Local Similarity 88.3%; Pred. No. 2.8e-76; Matches 159; Conservative 10; Mismatches 11 셤 P 원 8 $\ddot{\delta}$

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SEQUENCE FROM N.A.
MEDLINE=94186155; PubMed=8138250;
Shrestha S.M., Tsuda F., Okamoto H., Tokita H., Horikita M.,
Tanaka T., Miyakawa Y., Mayumi M.;
"Hepatitis B virus subtypes and hepatitis C virus genotypes i
patients with chronic liver disease in Nepal.";
Hepatology 19:805-809 (1994).
EMBL, D16520; BAD404042.1; -.
GO; GO:0016021; C:integral to membrane; IEA.

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GO, GO:0019028; C:viral capsid; IEA.

R GO, GO:0019031; C:viral capsid; IEA.

R GO, GO:0019031; C:viral envelope; IEA.

R GO, GO:005198; F:structural envelope; IEA.

InterPro; IPR002521; HCV capsid.

R InterPro; IPR002521; HCV core.

R InterPro; IPR002531; HCV core.

R Pfam; PF01543; HCV core; I.

R Pfam; PF01543; HCV core; I.

R Pfam; PF01543; HCV core; I.

R Pfam; PF01560; HCV cory; II.

R Pfam; PF01660; HCV cory; 
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Tokita H., Shrestha S.M., Okamoto H., Sakamoto M., Horikita M.,
Tizuka H., Shrestha S.M., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Nepal with novel genotypes and their
classification into the third major group.";
J. Gen. Virol. 75:931-936(1994).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-TON-2003 (TrEMBLrel. 24, Last annotation update)
Core, env, and part of E2/NS1 (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage, Flaviviridae;
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                                                                                                                                                                                                                                                                                                                                                 44839 MW; 809114E3D485C397 CRC64;
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Pred. No. 1.1e-75;
9; Mismatches 13;
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illarity 87.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                          415 AA;
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Best Local Similarity
Matches 158; Conserv
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SEQUENCE
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Q81552;
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Q81552
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Pfam; PF01543; HCV capsid; 1. Pfam; PF01542; HCV_core; 1. Pfam; PF01539; HCV_env; 1.

120 121 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMA 180 260 GHVDLLVGSATLCSALYVGDLCGAVFLVGQAFTFRPRRHTTVQTCNCSLYPGHITGHRMA 319 200 LYMLINDCSNSSIVYEAEDVILHMPGCVPCVQNGNTSECWTPATPTVAVRYAGATTASVR 1 VGAPVGGVARALAHGVRALEDGINFATGNIPGCSFSIFLLALFSCLIHPAASLEWRNTSG LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR Pfam; PF01560; HCV N31; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
NON TER 415 415
SEQÜENCE 415 AA; 44580 MW; 35F4EF4DF6F79C30 CRC64; .. 0 Length 415; 12; Indels Query Match

88.9%; Score 857; DB 2;
Best Local Similarity 86.7%; Pred. No. 1.7e-75;
Matches 156; Conservative 12; Mismatches 12; Search completed: December 1, 2004, 23:44:13 Job time: 195 secs 415 AA; 61 SHAMES & a. δ g 8

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December 1, 2004, 23:35:24; Search time 38 Seconds (without alignments) 455.764 Million cell updates/sec
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964
1 VGAFVGGVARALAHGVRALE......TVQTCNCSLYPGHLSGHRMA 180
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	enome	genome polyprotein	enome	enone	enone			Po1	genome polyprotein	g o	genome polyprotein	pol	enome p	DQ.	genome polyprotein	enome poly		hypothetical prote	genome polyprotein	genome polyprotein	enone	genome polyprotein	olypr	olyp	olypro	polyprotein - hepa	genome polyprotein		епоше
ID	PC1304	S41288	PC2061	PC1305	PC1303	PC2060	PC1284	S18032	319876	S18030	GNWVIC	GNWVCH	S12707	GNWVTW	S18031	GNWVCJ	A44150	PN0677	GNWVC3		~	JH0711	01	-	S19875	JQ1926	\sim	JC5620	
DB	7	N	(7	CI	N	(7)	N	N	N	Н	Н	н	7	Н	N	Н	N	ď	Н	Н	Н	N	0	~	N	N	0	Н	N
Length	180	492	411	180	180	411	513	782	782	3010	3010	3011	441	3010	782	3010	513	787	3011	3011	3010	550	520	369	782	523	640	3014	322
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Score	964	960	955	951	948	923	733	731	728	727	724	723	722	722	721	721	717	717	717	717	715	714	713	712	711	708	703	999	664
Result No.		2	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	٦	20	21	22	. 23	24	25	26	27		

genome polyprotein genome polyprotein	genome polyprotein	genome polyprotein	envelope protein -	envelope glycoprot	envelope glycoprot	envelope glycoprot	genome polyprotein	polypeptide - hepa						
GNWVJ8 JQ0883	JQ0881	JQ1303	PC4407	PS0165	PS0164	PN0011	S32749	S32745	S25123	\$32746	S32743	832741	835630	PC2219
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67.9	65.	65	63	52	22	51	49	48	47	47	47	47	4	ď
	632 65.											457 47		227.5 2.

ALIGNMENTS

PERSULT 1 PC1304 PC1304 Grid and polyprotein core/E1 region (isolate BR36-9) - hepatitis C virus (strain type 3) (if C;Species: hepatitis C virus C;Species: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004 C;Accession: PC1304 R;Stuyver, L.; Van Arnhem, W.; Wyseur, A.; DeLeys, R.; Maertens, G. Biochem. Biophys. Res. Commun. 192, 635-641, 1993 A;Title: Analysis of the putative E1 envelope and NS4a epitope regions of HCV type 3. A;Reference number: PC1304 A;Accession: PC1304 A;Accession: PC1304 A;Accession: PC1304 A;Residues: 1-180 <stu> A;Residues: 1-180 <stu> A;Residues: 1-180 <stu> A;Residues: Dlood C;Superfamiltal source: blood C;Superf</stu></stu></stu>	Query Match 100.0%; Score 964; DB 2; Length 180; Best Local Similarity 100.0%; Pred. No. 1.7e-81; O. Gaps 0; Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 VGAPVGGVARALAGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG 60 O. GAPVGGVARALAGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG 60 Qy 61 LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120 Qy 61 LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120 Qy 121 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRWA 180 Db 121 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRWA 180 LX 121 SHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRWA 180	RESULT 2 841288 genome polyprotein - hepatitis C virus (fragment) NiContains: core protein; envelope protein; NS1 protein C;Species: hepatitis C virus C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004 C;Accession: 841288 R;Seelig, R. submitted to the EMBL Data Library, December 1993 A;Reference number: 841288 A;Accession: 841288 A;Accession: 841288 A;Molecule type: genomic RNA A;Residues: 1-492 <83E> A;Cross-references: UNIPROT: Q68870; EMBL:X76918
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Groome polyprotein N2 - hepatitis C virus

N; Contains: envelope protein E1; nonstructural protein E2/NS1

C; Species: hepatitis C virus

N; Contains: converse protein E1; nonstructural protein E2/NS1

C; Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C; Accession: PC2061

R; Li, JS.; Vitvitski, L; Tong, S.P; Trepo, C.

Biochem. Biophys. Res. Commun. 199, 1474-1481, 1994

A; Title: Identification of the third major genotype of hepatitis C virus in France.
A; Reference number: PC2060; MUID:94197744; PMID:8147893

A; Accession: PC2061

A; Molecule type: mRNA
A; Residues: 1-411 cLiJ>
A; Molecule type: mRNA
A; Residues: 1-411 cLiJ>
A; Cross-references: UNIPPCT:Q81813; GB:L12355; NID:9410169; PIDN:AAA20155.1; PID:9410170
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; capsid protein; envelope protein; glycoprotein;
C; Keywords: ATP; capsid protein E1 #status predicted cAPE>
F; 192-383/Product: envelope protein E2/NS1 #status predicted
F; 196,209,234,305,325/Binding site: carbohydrate (Asn) (covalent) #status predicted
                               poly#
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C;5pecies: hepatitis C virus
C;5pecies: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: PC1305
R;Struyver, L.; van Arnhem, W.; Wageur, A.; DeLeys, R.; Maertens, G.
Bicchem. Biophys. Res. Commun. 192, 635-641, 1993
A;Title: Analysis of the putative El envelope and NS4a epitope regions of HCV type A;Reference number: PC1300; MUID:93249436; PMID:7683463
A;Accession: PC1305
A;Molecule type: mRNA
                            protein;
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C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; envelope protein;
F;1:191/Product: core protein #status predicted <COR>
F;192-372/Product: envelope protein #status predicted <ENV>
F;373-492/Product: NSI protein (fragment) #status predicted
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                                                                                                                                                           Score 960; DB 2;
Pred. No. 1.1e-80;
2; Mismatches 0;
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Pred. No. 2.6e-80;
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ilarity 97.8%;
Conservative
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Best Local Similarity
Matches 178; Conserv
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Prize polyprotein core/El region (isolate HD10-2) - hepatitis C virus (strain type 3) (if c) species: hepatitis C virus
C; Accession: PC1303
R; Stuyver, L.; Van Arnhem, W.; Myseur, A.; DeLeys, R.; Maertens, G.
Biochem. Biochem. Biochem. Biochem: Biochem. Bio
                            A;Cross-references: UNIPROT:081277; DDBJ:D14596; NID:g303576; PIDN:BAA03445.1; PID:g3035; A;Experimental source: blood Csuperfamily: hepatitis C virus genome polyprotein C;Superfamily: hepatitis C virus genome polyprotein; polyprotein; transmembrane p: F;S3-64,74-84,91-103,109-118,155-164/Region: hypervariable region #status predicted F;125-154/Domain: transmembrane #status predicted <PMPA P;57,70,95,166/Binding site: carbohydrate (Asn) (covalent) #status predicted
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N;Contains: envelope protein E1; nonstructural protein E2/NS1
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: PC206
E;Li, J.S.; Vitvitski, L.; Tong, S.P.; Trepo, C.
Biochem. Biophys. Res. Commun. 199, 1474-1481, 1994
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Pred. No. 2.6e-80;
2; Mismatches 2
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Best Local Similarity 97.8
Matches 176; Conservative
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Matches 175; Conservative
A;Residues: 1-180 <STU>
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Length 782;

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genome polyprotein - hepatitis C virus (isolate JKS) (fragment)
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
A;Variety: isolate JKS
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S19876
B; Masaahi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
                                       A;Accession: $18032
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Everidues: 1-782 «HON»
A;Cross-references: UNIPROT:Q68952; EMBL:X61594
A;Cross-references: UNIPROT:Q68952; EMBL:X61594
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
C;Keywords: capsid protein #status predicted <MAT1>
F;1-191/Product: core protein #status predicted <MAT2>
F;384-733/Product: Nors/E2 protein #status predicted <MAT3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>
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A. Molecule type: genomic RNA
A. Residues: 1-782 < 400.
A. Experimental source: isolate JKS
C. Superfamily: hepatitis C virus genome polyprotein
C. Superfamily: hepatitis C virus genome polyprotein; glycoprotein; nonstructural programmental source: isolate JKS
C. Say Product: core protein #status predicted < MATI2>
F. 192-383 / Product: envelope protein 1 #status predicted < MATI2>
F. 192-383 / Product: nonstructural protein 2 (fragment) #status predicted < MATI4>
F. 344-782 / Product: nonstructural protein 2 (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 VGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPVSTYEVRNVSG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LYVLTNDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIR 120
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    VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG

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                                                                                                                                                                                                                                                                                                                                                                                                                 75.8%; Score 731; DB 2; 72.2%; Pred. No. 2.1e-59; iive 24; Mismatches 26.
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llarity 72.8%; Pred. No. 3.9e-59;
Conservative 21; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 72.2'
Matches 130, Conservative
                A; Reference number: S18029
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518032
genome polyprotein - hepatitis C virus (isolate JX4) (fragment)
N Contains: core protein, envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
A;Variety: isolate JX4
C;Date: 30-Unn-1992 #sequence_revision 30-Unn-1992 #text_change 09-Jul-2004
C;Accession: S18032
R;Honda, M.; Kanneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
Sibmitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus isd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
PO1284
PO1284
Specials inepatitis C virus (isolate HC-J4) (fragment)
C;Specials hepatitis C virus
C;Specials hepatitis C virus
C;Specials hepatitis C virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
D;Date: The S'-terminal sequence of the hepatitis C virus genome.
A;Reference number: PC1284 MUID: 91013116; PMID: 2170712
A;Recession: PC1284
A;Molecule type: genomic RNA
A;Residues: 1-513 - OCRA>
A;Residues: 1-513 - OCRA>
A;Residues: 1-513 - OCRA>
A;Residues: C virus genome polyprotein
A,Title: Identification of the third major genotype of hepatitis C virus in France.
A,Reference number: PC2060, MUID:94197744; PMID:8147893
A,Accession: PC2060
A,Molecule type: MRNA
A,Residues: 1-411 < LIJ3
A,Cross-references: UNIPROT:081489
C,Superfamily: hepatitis C virus genome polyprotein
C,Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; C,Keywords: ATP; capsid protein E1 #status predicted < SPD>
F,384-411/Product: envelope protein E2 MSN1 #status predicted < NPB>
F,384-411/Product: nonstructural protein E2/MSN1 #status predicted < NPB>
F,196,209,234,305,325/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1-3010 <HON>
A; Residues: 1-3010 <HON>
A; Cross-references: UNIPROT: Q68949; EMBL: X61596; NID: 959478; PIDN: CAA43793.1; PID: 959479
A; Experimental source: isolate JX1 from an individual
A; Experimental source: isolate JX1 from an individual
A; Honda, M.; Kanako, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 128, 163-169, 1993
A; Ritle: Sequence analysis of putative structural regions of hepatitis C virus isolated
A; Reference number: A48332; MUID: 93119270; PMID: 8380322
                                                                                                                                             C,Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C,Accession: S18030, S31570, A4832; S18029
R;Honda, M.; Kaneko, S.; Massahi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A,Description: A whole genome of hepatitis C virus cDNA was isolated from a single patie
A,Reference number: S18028
A,Accession: S18030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fill6-1319/Region: DEXH motif
Fils6-1862/Product: nonstructural protein NS4a #status predicted <N4A>
Fils6-1962/Product: nonstructural protein NS4b #status predicted <N4B>
Fils6-2013/Product: nonstructural protein NS5 #status predicted <NS5>
Fils014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
Fils6,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate (As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome polyprotein - hepatitis C virus
N;Contains: capsid protein C; envelope protein N; hepacivirin (EC 3.4.21.98) (nonstructy protein NS4s; nonstructural protein NS4s; nonstructural protein NS5;
C;Species: hepatitis C virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A38465
R;Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.; J. Virol. 65, 1105-1113, 192
A;Title: Structure and organization of the hepatitis C virus genome isolated from human A;Reference number: A38465; MUDD:91140698; PMID:1847440
genome polyprotein - hepatitis C virus (isolate JK1)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu protein N94s, nonstructural protein NS5.
C;Species: hepatitis C virus
A;Variety: isolate JK1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.4%; Score 727; DB 1; 71.7%; Pred. No. 1.9e-58; ive 24; Mismatches 27
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Best Local Similarity 71.7%;
Marches 129; Conservative
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A,Modecule type: genomic RNA
A,Residues: 1.3010 <TAK>
A,Residues: 1.3010 <TAK>
A,Residues: 1.3010 <TAK>
A,Cross-references: UNIPROTIPEG663; EMBL:M58335; NID:g329770; PIDN:AAA72945.1; PID:g32977;
C,Superfamily: hepatitis C virus genome polyprotein
C,Superfamily: hepatitis C virus genome polyprotein
C,Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural
C,Keywords: ATP; capsid protein M #status predicted <REPA
F)115/Product: envelope protein M #status predicted <REPA
F)115/Product: major envelope protein MS1 #status predicted <NS1>
F)190-729/Product: nonstructural protein NS1 #status predicted <NS2>
F)1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>
F)1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>
F)117/Region: nucleotide-binding motif A (P-loop)
F)1186-1319/Region: nucleotide-binding motif B
F)11616-1862/Product: nonstructural protein NS4# #status predicted <NS5>
F)1863-2013/Product: nonstructural protein NS5# #status predicted <NS5>
F)196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1235,2041,2077,223
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A, Residues: 1-3011 - 4 NIC-
A, Robedues: 1-3011 - 4 NIC-
A, Robedues: 1-3011 - 4 NIC-
A, Residues: 1-3011 - 4 NIC-
A, Residues: 1-3011 - 4 NIC-
A, Cross-references: UNIRROT: P27958, GB: M67463; NID: G329737; PIDN: AAA45534.1; PID: G329738
R, Inchausge, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
R, Inchausge, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
A, Title: Genomic structure of the human prototype strain H of hepatitis C virus: comparis A, Reference number: A41546; MUID: 92052256; PMID: 1658800
A, Contents: annotation
A, Note: neither amnotation
A, Note: neither amnotation
C, Superfamily: hepatitis C virus genome polyprotein
C, Superfamily: hepatitis C virus genome
C, Superfamily: hepatitis C virus
C, Superfamily: hepatitis C virus
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C, Superfamily: hepati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŭ
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A;Description: Genomic structure of the human prototype strain H of hepatitis C virus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o,
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
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Matches 128;
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C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural F;1-115/Product: capsid protein C #status predicted <CPN F;116-191/Product: envelope protein M #status predicted <CPN F;192-899/Product: major envelope protein E #status predicted <ARE>
F;192-189/Product: nonstructural protein NS1 #status predicted <NRS>
F;30-729/Product: nonstructural protein NS2 #status predicted <NRS>
F;100-1006/Product: nonstructural protein NS2 #status predicted <NRS>
F;131-1317/Region: mucleotide-binding motif A (P-loop)
F;131-1317/Region: mucleotide-binding motif A (P-loop)
F;131-1319/Region: predicted binding motif B F;181-1319/Region: predicted constructural protein NS4 #status predicted <NRS>
F;1863-2013/Product: nonstructural protein NS4 #status predicted <NRS>
F;1863-2013/Product: nonstructural protein NS5 #status predicted <NRS>
F;1910/Product: nonstructural protein NS5 #status predicted <NRS>
F;1910/Product = NRS **
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N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
A;Variety: isolate JK2
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S18031
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Pescription: Sequence analysis of putative structural regions of Hepatitis C Virus iso.
A;Reference number: S18029
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Alkolecule type: genomic RNA
A.Rosidues: 1-782 eAGN>
A.Rosidues: 1-782 eAG
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74.8%; Score 721; DB 2; Length 78
Best Local Similarity 72.2%; Pred. No. 1.7e-58;
Matches 130; Conservative 21; Mismatches 29; Indels
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Best Local Similarity 71.15
Matches 128, Conservative
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             F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,23
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S12707
Nicontains: core protein; envelope protein
Nicontains: core protein; envelope protein
CiSpecies: hepatitis C virus
CiSpecies: hepatitis C virus
CiSpecies: 10-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
CiAccession: 512707
Nucleic Acids Res. 18, 4626, 1990
A.Pitle: Nucleotide sequence of core and envelope genes of the hepatitis C virus genome A.Reference number: S12707; MUD: 90356432; PMID:2117749
A.Accession: S12707
A.Accession: S12707
A.Residues: 1-441 - TAKs
A.Residues: 1-441 - TAKs
Cicosa-references: UNIPROT:Q81776; EMBL:D00574; NID:g221656; PIDN:BAA00452.1; PID:g221656; Superfamily: hepatitis C virus genome polyprotein
C; Reywords: polyprotein
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BN Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructure protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C; Species: hepatitis C virus
C; Species: hepatitis C virus
C; Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C; Accession: A4024
B; Chen, D-U; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen, D.S.
A; Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the A; Reference number: A40244, MUID:92230206; PMID:1314449
A; Residence or Companie C virus genome polyprotein
C; Superfamily: hepatitis C virus genome polyprotein
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SEQUENCE FROM N.A.

SEQUENCE 9249436; PubMed=7683463;
STUYVER I., Arnhem W.V., Myseur A., Deleys R., Maertens G.;
STUYVER I., Arnhem W.V., Myseur A., Deleys R., Maertens G.;
STUYVER I., Arnhem W.V., Myseur A., Deleys R., Maertens G.;
STUYVER I., Annalysis of the putative El envelope and NS4a epitope region of HCV

TYPE 3."

Elechem. Biophys. Res. Commun. 192:635-641(1993).

REMBL, D14559; BAA03448-1; -.

REMBL, D14559; BAA03448-1; -.

ROJ GO:0016021; C:integral to membrane; IEA.

GO, GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0015198; F:structural molecule activity; IEA.

RIMEPPO; IPRO02519; HCV_core.

RIMEPPO; IPRO02519; HCV_core.

RIMEPPO; IPRO052519; HCV_core.

Pfam: PF01542; HCV_core.

ROT GO:001539; HCV_core.

ROT GO:001539; HCV_core.

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Heparitis C virus.
Heparitis S SRNA positive-strand viruses, no DNA stage; Flaviviridae;
Heparoivirus.
NCBI_TaxID=11103;
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180 AA; 18934 MW; 15FEE3DED5481693 CRC64;
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Q81278;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Core protein-envelope 1 protein (Fragment).
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Maximum DB seq length: 2000000000
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Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF010099; Viral RdRP; 1.
SWART; SM00487; DEXDC; 1.
PROSTIE; PS00190; CYTOCHROME C; UNKNOWN 1.
Cost protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                          "Full-length sequence of the genome of hepatitis C virus type 3a: comparative study with different genotypes.";
J. Gen. Virol. 75:3279-3284(1994).
EMBL; D28917; BAAG6044.1;
HSSP; P27958; 1HEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROS GO: 6016021; CIINTEGRAI to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral envelope; IEA.

GO; GO:0009026; F:ATP binding; IEA.

GO; GO:0009236; F:ATP dependent helicase activity; IEA.

GO; GO:0009236; F:RNA directed RNA polymerase activity; IEA.

GO; GO:0009236; F:Serine-type peptidase activity; IEA.

GO; GO:0006236; F:Serine-type peptidase activity; IEA.

GO; GO:0006508; F:Serine-type peptidase activit
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                                                                                  Last sequence update)
Last annotation update)
     PRT; 3021 AA.
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InterPro; 1PR004109; Peptidase S29.
InterPro; 1PR004109; Peptidase S29.
InterPro; 1PR004003; Pept U39 HCV NS2.
InterPro; 1PR007094; RNA_DO1_DS P5.
InterPro; 1PR007094; RNA_DO1_PSvir.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01549; HCV_car; 1.
Pfam; PF01589; HCV_env; 1.
Pfam; PF01589; HCV_env; 1.
Pfam; PF01589; HCV NS2; 1.
                                                         Created)
                                                                                                                                                                                                                                                                                                             STRAIN=K3a;
MEDLINE=95053917; PubMed=7964640;
MEDLINE=95053917; PubMed=7964640;
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IPR002166; HCV RdRP.
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PR001490; HCV_NS4b.
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C . Q81495
C . Q81495,
T .01-NOV-1996 (TrEMBLrel. 01, C:
T .01-NOV-1996 (TrEMBLrel. 01, Le
T .01-NOV-1996 (TrEMBLrel. 01, Le
E . Polyprotein.
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                                                                                                                                                                                                                                NCBI_TaxID=11103;
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InterPro; IE
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InterPro; II
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9 ARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSGLYVLTNDC

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80 VILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIRSHVDLLVGAATMCSALYVG 139
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KEDINES_25101041; PubMed=12624035;

KEDINES_25101041; PubMed=12624035;

Corbet S., Bukh J., Heinsen A., Fonsgaard A.;

Corbet S., Bukh J., Heinsen A., Fonsgaard A.;

Transcriptase PCR assay with sequencing and its use in determining subtype distribution among Danish patients.";

J. Clin. Microbiol. 4:1091-1100(203).

E. Microbiol. 4:1091-1100(203).

E. Gol, GO.0016011; C.:integral to membrane; IEA.

R. GO, GO.0019028; C.:viral capsid; IEA.

R. GO; GO.0019011; C.:viral envelope; IEA.

R. GO; GO:0019029; F.:structural molecule activity; IEA.

InterPro; IPR002519; HCV_env.

InterPro; PR01539; HCV_env.

Transmembrane.

Transmembrane.
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                                                                                                                                                                                                                                           080KSO;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Polyprotein (Fragment)
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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117 117
117 AA; 12652 MW; 7329E0E12EEB4D20 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Core protein-envelope 1 protein (Fragment).
Name=core-E1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.6%; Score 91; DB 2; Let 100.0%; Pred. No. 7.2e-83; iive 0; Mismatches 0;
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Blochem: Biophys. Res. Commun. 192:635-641(1993).
EMBL: D14603; BAA03452.1; -.
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Best Local Similarity
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NCBI_TaxID=11103;
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Q81279;
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140 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG 199
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Obergoade (FEB-1994) to the EMBL/GenBank/DDEJ databases.

Submitted (FEB-1994) to the EMBL/GenBank/DDEJ databases.

BRIEL; D14305; BAA03251.1; -.

BRIEL; D14305; BAA03251.1; -.

BRIEL; D14305; BAA03251.1; -.

CO; GO:0019028; C: Virtal capsid; IEA.

CO; GO:0019028; C: Virtal capsid; IEA.

CO; GO:0005198; F: Structural molecule activity; IEA.

CO; GO:0005198; F: Core.

CO; GO:0005198; F: Structural molecule activity; IEA.

Coat protein; How Core; I.

Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

COAT protein; Envelope protein; Glycoprotein; C.

COAT protein; Tansmembrane.

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MEDLINE=94065664; PubMed=7504073;
Okamoto H., Tokita H., Sakamoto M., Horikita M., Kojima M., Iizuka H.,
Mishiro S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
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Hepacivirus.
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                                       Length 503;
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48.3%; Score 87; DB 2; Length 503
Best Local Similarity 100.0%; Pred. No. 2.5e-78;
Matches 87; Conservative 0; Mismatches 0; Indels
                                       Query Match
48.3%; Score 87; DB 2; Length 503
Best Local Similarity 100.0%; Pred. No. 2.5e-78;
Matches 87; Conservative 0; Mismatches 0; Indels
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384 >503 E2/NS1.
503 503 AA, 54822 MW, 24B9CCB7987FB94B CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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E2/NS1.
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Hepatitis C virus.
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REMBL; D1431; BAA0325 C. Lie Endly Combound; DDC Caracasses.

R CO; GO:0016021; C:intral capsid; DEA.

R CO; GO:0019031; C:viral capsid; DEA.

R CO; GO:0019031; C:viral envelope; DEA.

R CO; GO:005198; F:structural molecule activity; DEA.

R CO; GO:005198; F:structural molecule activity; DEA.

R InterPro; DR005251; HCV core.

R InterPro; DR005251; HCV core.

R InterPro; DR005251; HCV capsid.

R InterPro; DR005251; HCV capsid.

R InterPro; DR005251; HCV core; DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
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MEDLINE-94065664; PubMed=7504073;
Okamoto H., Tokita H., Sakamoto M., Horikita M., Kojima M., Iizuka H.,
Mishiro S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of the genomic sequence of type V (or 3a) hepatitis C virus isolates and PCR primers for specific detection."; J. Gen. Virol. 74:2385-2390(1993).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein (Fragment)
Hepatitis C virus.
Niruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBL TAXID=11103;
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R PIR; PC1303; PC1303.

R GO; GO: 0016021; C:integral to membrane; IEA.

GO; GO: 0019028; C:viral capsid; IEA.

GO; GO: 0019031; C:viral envelop; IEA.

GO; GO: 0019031; C:viral envelop; IEA.

R GO; GO: 0019031; HCV_core.

R InterPro; IPR00251; HCV_env.

R Pfam; PP01542; HCV_core; 1.

R Pfam; PP01539; HCV_env; 1.

R Coat protein; Envelope protein; Glycoprotein; Polyprotein;

M Coat protein; Envelope protein; Glycoprotein; Polyprotein;

R NON TER 18

D SEQÜENCE 180 AA; 19005 MW; F76270697B0C04F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.3%; Score 87; DB 2; Length 180; 100.0%; Pred. No. 1.1e-78; Live 0; Mismatches 0; Indels
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Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
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192 383 E.
384 >503 E2/NS1.
503 AA; 54531 MW; 2PE38EC30F779229 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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199

200 LYVLTNDCSNSSIVYEADDVILHTPGC 226

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PROSITE; PS00190; CYTOCHROWE C; UNKNOWN 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.

SEQUENCE 3021 AA; 328905 NW; D786133B33030CD CRC64;
                                                                                                                                                                                                    Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GG; GO:0016021; Cintegral to membrane; IEA.

GG; GO:0019028; C:viral capsid; IEA.

GG; GO:0019028; C:viral envelope; IEA.

GG; GO:0019024; F:ATP binding; IEA.

GG; GO:0008026; F:ATP binding; IEA.

GG; GO:0008125; F:RNA binding; IEA.

GG; GO:0008136; F:RNA-directed RNA polymerase activity; IEA.

GG; GO:0008136; F:serine-type peptidase activity; IEA.

GG; GO:0006198; F:structural molecule activity; IEA.

GG; GO:0006198; F:structural molecule activity; IEA.

GG; GO:0006199; F:structural molecule activity; IEA.

GG; GO:0006199; F:structural molecule activity; IEA.

GG; GO:000979; P:viral genome replication; IEA.

GG; GO:0019079; P:viral genome replication; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Lype 3a;
Shukla D.D., Chaturvedi S., Cao J.Y., Hoyne P.A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; APO46866; AAC03058.1; -.
HSSP; P27958; 1HEI.
                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                     PRT; 3021 AA.
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InterPro; IPRO04109; Peptidase S29.
InterPro; IPRO04109; Peptidase S29.
InterPro; IPRO09003; Pept_U39_HCV NS2.
InterPro; IPRO07095; RNA_DOI_DS_PS_
InterPro; IPRO07095; RNA_DOI_PS_IR.
Fam; PFO1549; HCV capsid; IPRO17094; RNA_DOI_PS_IR.
Pfam; PFO1549; HCV capsid; IPRO17096; RCV NS2; IPRO17096; HCV NS2; IPRO17096; HCV NS2; IPRO17096; HCV NS2; IPRO170909; HCV NS4; IPRO1709; HCV NS5; IPRO1709; IPRO1709; HCV NS5; IPRO1709; HCV NS5; IPRO1709; HCV NS5; IPRO1709; HCV NS5; IPRO1709; IPRO1709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000345; CytC_heme_BS
InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR002522; HCV capsid.
PR002521; HCV_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPRO02519; HCV—env.
IPRO02531; HCV NS1.
IPRO00745; HCV NS4a.
IPRO01490; HCV NS4b.
IPRO02868; HCV NS5a.
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                                                                                                        01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26,
                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11103;
                                                                                                                                                                                                 Polyprotein.
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                                                     . 092933
RESULT 7
                             092933
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LYVLTNDCSNSSIVYEADDVILHTPGC 87

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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Serum;
TISSUE=Serum;
Subalid R., Weber P., Seeling H.P., Ledger N., Bottner C., Renz M.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X76918; CAA54244.1; -.
PIR; PC1307; PC1307.
                                                                                                                                                                                                                                    R PIR; P00601; P00401.

R PIR; P00601; P00804.

R PIR; S41288; S41286.

R HSSP, P27958 ; JA12.

R GO; GO:0019021; C:integral to membrane; IEA.

GO; GO:0019021; C:intal capsid; IEA.

R GO; GO:000524; F:ATP binding; IEA.

R GO; GO:000524; F:ATP-dependent helicase activity; IEA.

R GO; GO:0003722; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0005286; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0005298; F:Structural molecule activity; IEA.

R GO; GO:0005299; F:structural molecule activity; IEA.

R GO; GO:0005599; P:viral genome replication; IEA.

R GO; GO:0019079; P:viral genome replication; IEA.
                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Genes for core, envelope and NSI proteins.
                        PRT; 3021 AA
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IPR002518; Pept U39 HCV NS2.
IPR007095; RNA pol DS PS.
IPR007094; RNA pol PSvir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR004109; Peptidase S29.
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IPR002521; HCV core.
IPR002519; HCV env.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPRO02531, HCV NS1.
IPRO0745; HCV NS4a.
IPRO01490; HCV NS4b.
IPRO02868; HCV NS5a.
IPRO02166; HCV RGRP.
                        PRELIMINARY;
                                                                                                                                        NCBI_TaxID=11103;
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InterPro;
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InterPro;
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InterPro;
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                                    068870;
                        068870
RESULT 8
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LEAD PRO1539; HCV env; 1.

DR Pfam; PF01539; HCV env; 1.

DR Pfam; PF01539; HCV NS1; 1.

DR Pfam; PF01539; HCV NS2; 1.

DR Pfam; PF01001; HCV NS3; 1.

DR Pfam; PF01001; HCV NS4; 1.

DR Pfam; PF01001; HCV NS4; 1.

DR Pfam; PF010098; Viral, RGRP; 1.

DR PRO3TTE; PS00439; PEROXIDASE; 1.

DR PRO3TTE; PS00439; PEROXIDASE; 1; UNKNOWN 1.

DR PRO5TTE; PS00439; PEROXIDASE; 1; UNKNOWN 1.

RW POLYPOTOTION; Brvelope protein; Rometructural protein; RW POLYPOTOTION; RM POLYPOTOTION; RM POLYPOTOTION; RM POLYPOTOTION; RM RM 1013 1663 NS3.

PT CHAIN 1013 1663 NS3.

PT CHAIN 1019 NS4a.

PT CHAIN 1019 NS4a.
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MEDLINE=97201609; PubMed=9049395;
AND DOORN L.J., Kleter G.E., Stuyver L., Maertens G., Brouwer J.T.,
Aschalm S.W., Heijtink R.A., Quint W.G.V.;
Schalm S.W., Heijtink R.A., Quint W.G.V.;
Schalm S.W., Heijtink R.A., Quint W.G.V.;
I. "Sequence analysis of heparitis C virus genotypes 1 to 5 reveals
IT multiple novel subtypes in the Benelux countries.";
J. Gen. Virol. 76:1871-1876(1995).

EMBL; L39289; AAA67821.1;
OG GO:0016021; C:integraphic membrane; IEA.

RO; GO:0016021; C:viral capabid, IEA.

RO; GO:0019031; C:viral envelope; IEA.

RO; GO:005191; R:structural molecule activity; IEA.

RICHERPO; IPR002521; HVV. Core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG
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Hepacivirus; Hepatitis C virus type 3.
NCBI_TaxID=31652;
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MEDLINE=95052487; PubMed=7525693;
van Doorn L.J., Kleter B., Stuyver L., Maertens G., Brouwer H.,
schalm S., Heijtink R., Quint W.;
"Analysis of hepatitis C virus genotypes by a line probe assay and
correlation with antibody profiles.";
J. Hepatol. 21:122-129(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.3%; Score 87; DB 2; Length 3021; 100.0%; Pred. No. 1.1e-77; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 383 E1.
384 735 E2/N81.
3021 AA, 329575 MW; 38712CCBC0C19562 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Precursor protein (Fragment).
Hepatitis C_virus type 3a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 LYVLTNDCSNSSIVYEADDVILHTPGC 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.
NS4b.
NS5a.
NS5a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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1979
2431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Q68728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFSCLIHPAASLEWRNTSG 60
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polyprotein.
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECURATE FROM N.A.

CKAMCIO H.;

SUDMITTED (SEP-1993) to the EMBL/GenBank/DDBJ databases.

SHEL; D1763; BAA04609.1; -.

PIR; PGO401; PGO401.

PIR; PGO401; PGO401.

PIR; PGO1019028; Civiral capsid; IEA.

GO; GO:0019028; Civiral capsid; IEA.

GO; GO:0019028; Civiral capsid; IEA.

GO; GO:0019028; Civiral capsid; IEA.

GO; GO:000324; F:ATP-binding; IEA.

GO; GO:0003254; F:RAP binding; IEA.

GO; GO:000326; F:RAP-dependent helicase activity; IEA.

RO; GO:000326; F:RAP-dinding; IEA.

GO; GO:000326; F:RAP-dinding; IEA.

RO; GO:000326; F:RAP-dinding; IEA.

RICE-PRO; IPRO02521; HCV_capsid.

RICE-PRO; IPRO02519; HCV_RAP.

RICE-PRO; IPRO02619; HCV_RAP.

RICE-PRO; IPRO02016; HCV_RAP.

RICE-PRO; IPRO02016; HCV_RAP.

RICE-PRO; IRROPO0019; PEDE SET GYS.

RICE-PRO; IRROPO0019; ROM PEDE SET GYS.

RICE-PRO; ROM RA
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0
                                                                                                                                                                                                                                                                                                                                   Length 3021;
                                                                                                                                    1979 2430 NS5a protein.
2431 3021 NS5b protein.
192 383 envelope protein.
384 735 NS1 protein.
3021 AA, 329093 MW, BF2B499AA55A58CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sakamoto M.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O81258;
U-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                               48.3%; Score 87; DB 2; Le
100.0%; Pred. No. 1.1e-77;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 3021 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LYVLTNDCSNSSIVYEADDVILHTPGC 87
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                       CHAIN
CHAIN
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SEQUENCE
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Best Local S:
Matches 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 LINDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIRSHV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 VTPTVAVKYVGATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGGAFFRFRRHQTV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 LINDCSNSSIVYEADDVILHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIRSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 VTPTVAVKYVGATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTV
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Envelope protein (Fragment).

Hepatitis C virus.

Viruses, ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepativirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=3a;
MaDille=95146953; PubMed=7844535;
Greene W.K., Cheong M.K., Ng V., Yap K.W.;
"Prevalence of hepatitis C virus sequence variants in South-Bast
Pfam; PF01542; HCV_core; 1.

Pfam; PF01539; HCV_env; 1.

Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.

NON TER 1 1 1 1 1 CHAIN <1 32 CORE protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Gen., Virol. 76:211-215(1995).

EMBL; U14212; AAC53901.1; -.

EMBL; U14212; AAC53901.1; -.

GO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR002519; HCV env.

Pfam; PF01539; HCV env.

Pfam; PF01539; HCV env.

Pfam; PF01539; MCV env.

Pfam; PF01539; MCV
                                                                                                                                                                                                                                                                                                                                                   Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.3%; Score 78; DB 2; Length 128 ilarity 100.0%; Pred. No. 8.7e-70; Conservative 0; Mismatches 0; Indels
                                                                                                                                       1 1 core protein.
33 >149 el protein.
149 149 MW; 7D48172927B98021 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 128
128 AA; 13786 MW; FAA94C46DF80D0DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                47.2%; Score 85; DB 2; L ilarity 100.0%; Pred. No. 9.2e-77; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 DLLVGAATMCSALYVGDMCGAVFLV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 DLLVGAATMCSALYVGDMCGAVFLV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 QTCNCSLYPGHLSGHRMA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 85;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 85
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NON TER
SEQUENCE
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Q68176
       SFFFF
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128 AA.

PRT;

PRELIMINARY;

068178 068178;

RESULT 12 Q68178 ID Q68171 AC Q68171

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51 VIPIVAVKYVGATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 VIPTVAVKYVGATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEVOLUTION OF hepatitis C virus in blood donors and their respective recipients.";
J. Gen. Virol. 84:441-446(2003).

Gen. Virol. 84:441-446(2003).

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0015198; F:structural molecule activity; IEA.

InterPro; IPR002519; HCV env. I.
                                                                                 Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                            STRAIN=3a;
MEDILNE=55.46953; PubMed=7844535;
Greene W.K., Cheong M.K., Ng V., Yap K.W.;
"Prevalence of hepatitis C virus sequence variants in South-East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILME=22447295; Pubmed=12560577;
Cantaloube J.F., Blagini F., Attoui H., Gallian P., de Micco P.,
de Lamballerie X.;
                                                                                                                                                                                                                                                                                                                                 EMBL, U14214, A053903.1; --
EMBL, U14214, A053903.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR002519; HCV env.
Pfam; PF01539; HCV env. 1.
Coat protein; Envelope protein; Glycoprotein; Polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01539; HCV env. I.
Coat protein; Envelope protein; Glycoprotein; Polyprotein;
NON TER 119 119 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AA, 13835 MW, 04D7C339AB2AECSF CRC64;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Envelope protein El (Fragment).
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 43.3%; Score 78; DB 2; L
1 Similarity 100.0%; Pred. No. 8.7e-70;
78; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 AA.
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                                                                                                                                                                                                                                                                                                                    J. Gen. Virol. 76:211-215(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 QTCNCSLYPGHLSGHRMA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 QTCNCSLYPGHLSGHRMA 180
                                                                 Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                NCBI_TaxID=11103;
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NCBI_TaxID=11103;
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                                                                                                                                          111 YVGATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLY 170
                                                                                                                                                                        21 YVGATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRHQTVQTCNCSLY 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=3a,

MEDLINE=95146953; PubMed=7844535;

MEDLINE=95146953; PubMed=7844535;

A Greene W. K., Cheong M.K., Ng V., Yap K.W.;

T Asia...;

L Gen. Virol. 76:211-215(1995).

EMBL; U14221; AAC53910.1; -. membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral envelope; IEA.

R DITEPPRO; IPR002519; HCV env.

R Pfam; PF01539; HCV env.

R Pfam; PF01539; HCV env.

M Coat protein; Envelope protein; Glycoprotein; Polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                 Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Core protein-envelope 1 protein (Fragment).
Name-core-El;
Heparitis C virus.
Heparitis C virus.
Heparitis Purses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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OBJUST

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38.9%; Score 70; DB 2; Length 128;
Best Local Similarity 100.0%; Fred. No. 9.3e-62;
Matches 70; Conservative 0; Mismatches 0; Indels
                                                Length 119;
                                              Query Match 38.9%; Score 70; DB 2; Length 119 Best Local Similarity 100.0%; Fred. No. 8.8e-62; Matches 70; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 128 AA; 13859 MW; E896D3166D861B4A CRC64;
  D69FCA6EC118462F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 AA
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     119 AA; 13004 MW;
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MUSINERS-92494345; PubMed=7683463;

RA MISINERS-92494345; PubMed=7683463;

RA MISINERS-92494345; PubMed=7683463;

RT 'Analysis of the putative El envelope and NS4a epitope region of HCV

RI 'Analysis of the putative El envelope and NS4a epitope region of HCV

RI BIOChem. Biophys. Res. Commun. 192:635-641(1993).

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